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OM protein - protein search, using sw model

Run on: October 9, 2002, 00:24:29 ; Search time 49.62 Seconds
(without alignments)
367.112 Million cell updates/sec

Title: US-09-786-130-1

Perfect score: 164
Sequence: 1 TPVSQTTATATASVSTKDP.....TLPTQELPSSHSPQGG 164

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

A.Geneseq_032802:*

- 1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
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- 8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
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- 11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
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- 18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	164	100.0	164	21	AAV83951
2	164	100.0	192	20	AAW80004
3	164	100.0	194	21	AAV82922
4	164	100.0	194	21	AAV83985
5	139	84.8	197	20	AAW80006
6	137	83.5	137	21	AAV83982
7	97	59.1	161	20	AAW80007
8	48	29.3	113	20	AAW80005
9	47	28.7	47	21	AAV83984
10	40	24.4	40	20	AAW80008
11	24	14.6	55	20	AAV12716

12	20	12.2	117	21	AAV83986
13	20	12.2	165	21	AAV83952
14	20	12.2	193	21	AAV83989
15	19	11.6	49	21	AAV83983
16	15	9.1	55	20	AAV12536
17	13	7.9	23	21	AAV83958
18	12	7.3	29	21	AAV83960
19	11	6.7	11	21	AAV83955
20	9	5.5	9	21	AAV83954
21	8	4.9	8	21	AAV83956
22	8	4.9	8	21	AAV83957
23	8	4.9	520	19	AAW79001
24	8	4.9	520	21	AAW23467
25	8	4.9	571	22	AAW27242
26	8	4.9	634	22	ABW6245
27	8	4.9	737	22	ABW28978
28	8	4.9	840	20	AAW93570
29	8	4.9	840	20	AAW93569
30	7	4.3	7	21	AAV83962
31	7	4.3	7	21	AAV83964
32	7	4.3	7	21	AAV83965
33	7	4.3	7	21	AAV83979
34	7	4.3	10	21	AAV83959
35	7	4.3	50	14	AAW42168
36	7	4.3	54	22	AAW82588
37	7	4.3	86	22	AAW9872
38	7	4.3	86	22	AAW43671
39	7	4.3	90	21	AAW16286
40	7	4.3	92	22	AAU56894
41	7	4.3	103	22	AAW82993
42	7	4.3	135	21	AAW82140
43	7	4.3	136	22	AAW91688
44	7	4.3	139	22	ABW08356
45	7	4.3	161	22	AAW82089

ALIGNMENTS

RESULT 1
AAV83951
AAV83951 standard; Protein: 164 AA.
AC AAV83951;
XX 28-JUL-2000 (first entry)
DT Human mature interleukin 18 binding protein.
DE
XX Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease.
XX Homo sapiens.
OS
XX
PN W0200012555-A1.
XX
XX 09-MAR-2000.
PD
XX 18-NOV-1998; 98WO-JP05186.
PF
XX 01-SEP-1998; 98JP-0247588.
PR 18-NOV-1998; 98JP-0327914.
XX
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PA Torioge K, Tanai M, Kurimoto M;
XX WPI: 2000-237850/20.
XX N-PSDB: AAI11002.
PT Interleukin 18-binding protein with activity of regulating
PT physiological actions of interleukin 18, useful as regulator and drug

PT for sensitivity diseases and organ rejection and in treating diseases
 PT due to excess immune reaction
 XX Claim 1; Page 44-45; 71pp; Japanese.
 XX
 CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
 CC from humans or mice which act as regulators and drugs for sensitivity
 CC diseases and organ rejection and in treating diseases due to excess
 CC immune reaction, e.g. in slowing down rejection after organ transplant,
 CC and in treating autoimmune diseases. This sequence represents the mature
 CC human interleukin 12 binding protein.
 XX
 SQ Sequence 164 AA;
 Query Match 100.0%; Score 164; DB 21; Length 164;
 Best Local Similarity 100.0%; Pred. No. 5.3e-158;
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPVSQTTTAAATASVRSKDPSPQPPVFPAAKCPALVETWPEVEVPLNGTSLSCVACS 60
 DB 1 tpsqgtlaataasvrsstkdpqppvfpaakcpalevtwpevevplngtislscvacs 60
 QY 61 RFPNFSILYWLNGSFIENHPGRMEGSTSRREGSTGTQCKALVLEOLTPALHSTNFSC 120
 DB 61 rfpnfsilywlngsfienhpgrlmgsgstsrregstgtqckalvleoltpalhstnfsc 120
 QY 121 VLVDPQVQVRHVLAQLMAGLRATLPPTQEALPSSHSSPOOOG 164
 DB 121 vlvdpqvwvrhvlalqlmaglratlptqgealpsshsspqoog 164
 DB 121 vlvdpqvwvrhvlalqlmaglratlptqgealpsshsspqoog 164
 RESULT 2
 AAW98004
 ID AAW98004 standard; Protein; 192 AA.
 XX
 AC AAW98004;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Human interleukin-18 binding protein splice variant IL-18BPa.
 XX
 KW Interleukin-18 binding protein; IL-18BP; IL-18BPa; splice variant;
 KW human; autoimmune disease; inflammation; diabetes; pancreatitis;
 KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
 KW psoriasis; inflammatory bowel disease; multiple sclerosis;
 KW ischemic heart disease; ischemic brain injury; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..28 /note="signal peptide"
 FT Protein 29..192 /note="mature protein"
 FT
 FT
 XX
 WO9909063-A1.
 XX
 PD 25-FEB-1999.
 XX
 PF 13-AUG-1998; 98WO-IL00379.
 XX
 PR 22-JUL-1998; 98IL-0125463.
 PR 14-AUG-1997; 97IL-0121554.
 PR 27-AUG-1997; 97IL-0121639.
 PR 29-SEP-1997; 97IL-0121860.
 PR 06-NOV-1997; 97IL-0122134.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Dinarello C, Kim SH, Novick D, Rubinstein M;
 XX
 DR WPI; 1999-180975/15.

DR N-PSDB; AAX24749.
 XX
 PT New interleukin-18 binding protein - useful for treating human
 PT diseases, including autoimmune disease and inflammation
 XX
 PS Claim 3; Page 53-54; 100pp; English.
 XX
 CC The present sequence represents a human interleukin-18 binding
 CC protein (IL-18BP) splice variant designated IL-18BPa. This
 CC is one of 4 novel splice variants (see also AAW98005-07), all
 CC putative soluble proteins, encoded by cDNA clones (see AAX24749-52)
 CC detected following a screening of human peripheral blood monocyte,
 CC Jurkat T-cell, peripheral blood mononuclear cell and spleen cell
 CC cDNA libraries. IL-18BPa is the most abundant of the 4 splice
 CC variants and is a putative member of the immunoglobulin superfamily.
 CC Its first 40 residues perfectly match the N-terminal sequence of
 CC urinary IL-18BP (see AAW98008). IL-18BP polypeptides capable of
 CC binding IL-18 and/or modulating and/or blocking IL-18 activity are
 CC provided. Methods for their isolation and recombinant production,
 CC DNA vectors expressing them, vectors useful for their expression in
 CC humans and other mammals, and antibodies against them are also
 CC provided. IL-18BP polypeptides, and DNA encoding them, can be used
 CC to treat conditions requiring the protein (claimed). Conditions
 CC include autoimmune diseases, type I diabetes, rheumatoid arthritis,
 CC graft rejections, inflammatory bowel disease, sepsis, multiple
 CC sclerosis, ischemic heart diseases, ischemic brain injury, chronic
 CC hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is
 CC also useful for purifying IL-18 (claimed).
 XX
 SQ Sequence 192 AA;
 Query Match 100.0%; Score 164; DB 20; Length 192;
 Best Local Similarity 100.0%; Pred. No. 6.1e-158;
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPVSQTTTAAATASVRSKDPSPQPPVFPAAKCPALVETWPEVEVPLNGTSLSCVACS 60
 DB 29 tpsqgtlaataasvrsstkdpqppvfpaakcpalevtwpevevplngtislscvacs 88
 QY 61 RFPNFSILYWLNGSFIENHPGRMEGSTSRREGSTGTQCKALVLEOLTPALHSTNFSC 120
 DB 89 rfpnfsilywlngsfienhpgrlmgsgstsrregstgtqckalvleoltpalhstnfsc 148
 QY 121 VLVDPQVQVRHVLAQLMAGLRATLPPTQEALPSSHSSPOOOG 164
 DB 149 vlvdpqvwvrhvlalqlmaglratlptqgealpsshsspqoog 192
 RESULT 3
 AAY96292
 ID AAY96292 standard; protein; 194 AA.
 XX
 AC AAY96292;
 XX
 DT 16-AUG-2000 (first entry)
 XX
 DE Human IGFAM-4 immunoglobulin.
 XX
 KW Human; immunoglobulin; IGFAM-4; IGFAM; immune disorder; cancer;
 KW infection; inflammation; haematopoiesis; AIDS; allergy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..30 /label="signal_peptide"
 FT Protein 31..194 /label="IGFAM-4"
 FT
 FT
 XX
 PN WO200029583-A2.
 XX
 PD 25-MAY-2000.

XX 19-NOV-1999; 99WO-US27566.
XX
XX
PR 19-NOV-1998; 99US-0113635.
PR 22-DEC-1998; 98US-0113635.
PR 07-APR-1999; 99US-0128194.
XX
XX (INCY-) INCYTE PHARM INC.
XX
PI Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
PI Lu DAM, Lai P, Hillman JL, Yang J;
XX
XX WPI; 2000-387796/33.
DR N-PSDB; AAA27384.
XX
XX Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT protein is useful for preventing and treating disorders associated with
PT altered levels of the protein such as cancer, immune system disorders
XX
XX
PS Claim 1; Page 81; 105pp; English.
XX
XX The present sequence is the human immunoglobulin superfamily protein
CC IGFBP-4. Its gene was isolated from a cDNA library of prostate tumour
CC tissue. It is expressed in nervous, haematopoietic and immune and
CC cardiovascular tissue, where cancer and inflammation are common. The
CC gene, protein, its antibodies, agonists and antagonists are suitable for
CC diagnosing and treating many diseases, including cancer, immune system
CC disorders (such as inflammation, AIDS, allergies, anaemia,
CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
CC systemic lupus erythematosus and ulcerative colitis), complications of
CC cancer, haemodialysis and extracorporeal circulation, trauma and
CC haematopoietic cancer (such as leukaemia) and infections caused by
CC bacteria, viruses, fungi or parasites.
XX
XX Sequence 194 AA;
SQ

Query Match 100.0%; Score 164; DB 21; Length 194;
Best Local Similarity 100.0%; Pred. No. 6.2e-158;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TPVSOTTAATAASVSTDPGSPQPPVFPAAKQCPALVETWPEVPLNGTISTSCVACS 60
DB 31 TPVSQTLTAATAASVSTKDCPSPQPPVFPAAKQCPALVETWPEVPLNGTISTSCVACS 90
QY 61 RFPNFSILYWLGNCSFIEHLPGRLEWGSTSRERGSTGTOLKALVLEQITPALHSTNFSC 120
DB 91 RFPNFSILYWLGNCSFIEHLPGRLEWGSTSRERGSTGTOLKALVLEQITPALHSTNFSC 150
QY 121 VLVDPEQVYVQRHVLAQLWAGLRATLPTQDALPSSHSSPOOQG 164
DB 151 VLVDPEQVYVQRHVLAQLWAGLRATLPTQDALPSSHSSPOOQG 194

RESULT 4
AAV83985
ID AAV83985 standard; Protein; 194 AA.
XX
XX AAV83985;
XX
XX 28-JUL-2000 (first entry)
XX
XX Full length human interleukin 18 binding protein.
XX
XX Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease.
XX
XX Homo sapiens.
XX

FH Key Location/Qualifiers
FT Peptide 1..30
FT /label= signal_peptide
FT Protein 31..194
FT /label= "mature human IL-18 binding protein"
XX
XX WO200012555-A1.
XX
XX 09-MAR-2000.
XX
XX 18-NOV-1998; 98WO-JP05186.
XX
XX 01-SEP-1998; 98JP-0247588.
PR 18-NOV-1998; 98JP-0327914.
XX
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Torioge K, Tanai M, Kurimoto M;
PI
XX WPI; 2000-237850/20.
DR N-PSDB; AAA11007.
XX
XX
XX Interleukin 18-binding protein with activity of regulating
PT physiological actions of interleukin 18, useful as regulator and drug
PT for sensitivity diseases and organ rejection and in treating diseases
PT due to excess immune reaction
XX
XX Example 2; Page 63-64; 71pp; Japanese.
XX
XX The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC and in treating autoimmune diseases. This sequence represents the full
CC length human interleukin 12 binding protein.
XX
XX Sequence 194 AA;
SQ

Query Match 100.0%; Score 164; DB 21; Length 194;
Best Local Similarity 100.0%; Pred. No. 6.2e-158;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TPVSOTTAATAASVSTDPGSPQPPVFPAAKQCPALVETWPEVPLNGTISTSCVACS 60
DB 31 TPVSQTLTAATAASVSTKDCPSPQPPVFPAAKQCPALVETWPEVPLNGTISTSCVACS 90
QY 61 RFPNFSILYWLGNCSFIEHLPGRLEWGSTSRERGSTGTOLKALVLEQITPALHSTNFSC 120
DB 91 RFPNFSILYWLGNCSFIEHLPGRLEWGSTSRERGSTGTOLKALVLEQITPALHSTNFSC 150
QY 121 VLVDPEQVYVQRHVLAQLWAGLRATLPTQDALPSSHSSPOOQG 164
DB 151 VLVDPEQVYVQRHVLAQLWAGLRATLPTQDALPSSHSSPOOQG 194

RESULT 5
AAW98006
ID AAW98006 standard; Protein; 197 AA.
XX
XX AAW98006;
XX
XX 21-JUN-1999 (first entry)
XX
XX Human interleukin-18 binding protein splice variant IL-18BP.
XX
XX Interleukin-18 binding protein; IL-18BP; IL-18BPc; splice variant;
KW human; autoimmune disease; inflammation; diabetes; pancreatitis;
KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
KW psoriasis; inflammatory bowel disease; multiple sclerosis;
KW ischemic heart disease; ischemic brain injury; therapy.
XX
XX Homo sapiens.
XX

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XX Key Location/Qualifiers
FH Peptide 1..28
FT /note= "signal peptide"
FT Protein 29..197
FT /note= "mature protein"
PN WO9909063-A1.
PD 25-FEB-1999.
XX
XX 13-AUG-1998; 98WO-IL00379.
XX
XX 22-JUL-1998; 98IL-0125463.
XX 14-AUG-1997; 97IL-0121554.
XX 27-AUG-1997; 97IL-0121639.
XX 29-SEP-1997; 97IL-0121860.
XX 06-NOV-1997; 97IL-0122134.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Diarello C, Kim SH, Novick D, Rubinstein M;
XX WPI: 1999-180975/15.
XX N-PSDB: AAX24751.
XX
XX New interleukin-18 binding protein - useful for treating human
XX diseases, including autoimmune disease and inflammation
XX
XX Claim 3; Page 58-59; 100pp; English.
XX
XX The present sequence represents a human interleukin-18 binding
XX protein (IL-18BP) splice variant designated IL-18Bpc. This is one
XX four novel splice variants (see also AAW98004-07), all putative
XX soluble proteins, that are encoded by cDNA clones (see AAX24749-52)
XX detected following a screening of human peripheral blood monocyte,
XX Jurkat T-cell, peripheral blood mononuclear cell and spleen cell
XX cDNA libraries. IL-18Bpc is a low abundance variant. IL-18BP
XX polypeptides capable of binding IL-18 and/or modulating and/or
XX blocking IL-18 activity are provided, as are methods for their
XX isolation and recombinant production, DNA vectors expressing them,
XX and antibodies against them. IL-18BP polypeptides, and DNA encoding
XX them, can be used to treat conditions requiring the protein
XX (claimed). Conditions include autoimmune diseases, type I diabetes,
XX rheumatoid arthritis, graft rejections, inflammatory bowel disease,
XX sepsis, multiple sclerosis, ischemic heart diseases, ischemic brain
XX injury, chronic hepatitis, psoriasis, and chronic/acute
XX pancreatitis. IL-18BP is also useful for purifying IL-18 (claimed).
XX
XX Sequence 197 AA:
SQ
Query Match 84.8%; Score 139; DB 20; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.3e-132;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TPVSQTTAATASVRSKTPCPSPVPFPAKOCPALEVTWPEVEYPLNGTSLSCVACS 60
DB 29 tpsqgttaataasvrsktpcpqpvpfpaakcpalevtwpeveplngtstlscvacs 88
QY 61 RFPNFSILYWLNGSGFIEHLPGRLMGSTSRERGSGTGQCKALVLEQLTPALHSTNFSC 120
DB 89 rfpnfsilywlngsfiehlpgrlmgstsrergsgtgqckalvleqltpalhstnfsc 148
QY 121 VLVDPQOVQORHVLAQLW 139
DB 149 vlvdpqovvqrhvnlaqlw 167

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XX AAY83982;
AC 28-JUL-2000 (first entry)
XX
XX Human IL-18 binding protein 5' RACE fragment #1 encoded protein.
DE
XX Immunosuppressant; Interleukin 18 binding protein; IL18-BP; human; mouse;
XX regulator; drug; sensitivity disease; organ rejection; organ transplant;
XX autoimmune disease; rapid amplification of cDNA ends; RACE.
XX
XX Homo sapiens.
XX
XX WO200012555-A1.
XX
XX 09-MAR-2000.
XX
XX 18-NOV-1998; 98WO-JP05186.
XX
XX 01-SEP-1998; 98JP-0247588.
XX 18-NOV-1998; 98JP-0327914.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Toriigoe K, Tanial M, Kurimoto M;
XX WPI: 2000-237850/20.
XX N-PSDB: AAA11004.
XX
XX Interleukin 18-binding protein with activity of regulating
XX physiological actions of interleukin 18, useful as regulator and drug
XX for sensitivity diseases and organ rejection and in treating diseases
XX due to excess immune reaction -
XX
XX Example 2; Page 60-61; 71pp; Japanese.
XX
XX The invention relates to novel interleukin 18 (IL-18)-binding proteins
XX from humans or mice which act as regulators and drugs for sensitivity
XX diseases and organ rejection and in treating diseases due to excess
XX immune reaction, e.g. in slowing down rejection after organ transplant,
XX and in treating autoimmune diseases. This sequence represents the
XX protein encoded by the initial fragment isolated by a 5' RACE (Rapid
XX Amplification of cDNA Ends) reaction for the 5' end of the interleukin
XX 12 binding protein coding sequence.
XX
XX Sequence 137 AA:
SQ
Query Match 83.5%; Score 137; DB 21; Length 137;
Best Local Similarity 100.0%; Pred. No. 1e-130;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TPVSQTTAATASVRSKTPCPSPVPFPAKOCPALEVTWPEVEYPLNGTSLSCVACS 60
DB 1 tpsqgttaataasvrsktpcpqpvpfpaakcpalevtwpeveplngtstlscvacs 60
QY 61 RFPNFSILYWLNGSGFIEHLPGRLMGSTSRERGSGTGQCKALVLEQLTPALHSTNFSC 120
DB 61 rfpnfsilywlngsfiehlpgrlmgstsrergsgtgqckalvleqltpalhstnfsc 120
QY 121 VLVDPQOVQORHVLAQLW 137
DB 121 vlvdpqovvqrhvnlaqlw 137

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RESULT 6
AAW83982
ID AAY83982 standard; Protein; 137 AA.

RESULT 7
AAW98007
ID AAW98007 standard; Protein; 161 AA.
AC AAW98007;
XX
XX 21-JUN-1999 (first entry)
XX

```

DE Human interleukin-18 binding protein splice variant IL-18BPd.
XX
XX Interleukin-18 binding protein; IL-18BP; IL-18BPd; splice variant;
KW human; autoimmune disease; inflammation; diabetes; pancreatitis;
KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
KW psoriasis; inflammatory bowel disease; multiple sclerosis;
XX ischemic heart disease; ischemic brain injury; therapy.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..28
FT /note= "signal peptide"
FT Protein 29..161
FT /note= "mature protein"
XX
XX WO9909063-A1.
XX
XX 25-FEB-1999.
XX
XX 13-AUG-1998; 98WO-IL00379.
XX
XX 22-JUL-1998; 98IL-0125463.
XX 14-AUG-1997; 97IL-0121554.
XX 27-AUG-1997; 97IL-0121639.
XX 29-SEP-1997; 97IL-0121860.
XX 06-NOV-1997; 97IL-0122134.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX DiNarello C, Kim SH, Novick D, Rubinstein M;
PI WPI: 1999-180975/15.
XX N-PSDB; AAX24752.
XX
XX New interleukin-18 binding protein - useful for treating human
PT diseases, including autoimmune disease and inflammation
PT
XX Claim 3; Page 60; 100pp: English.
XX
XX The present sequence represents a human interleukin-18 binding
CC protein (IL-18BP) splice variant designated IL-18BPd. This is one
CC four novel splice variants (see also AAW98004-07), all putative
CC soluble proteins, that are encoded by cDNA clones (see AAX24749-52)
CC detected following a screening of human peripheral blood monocyte,
CC Jurkat T-cell, peripheral blood mononuclear cell and spleen cell
CC cDNA libraries. IL-18BPd is a low abundance variant. IL-18BP
CC polypeptides capable of binding IL-18 and/or modulating and/or
CC blocking IL-18 activity are provided, as are methods for their
CC isolation and recombinant production, DNA vectors expressing them,
CC vectors useful for their expression in humans and other mammals,
CC and antibodies against them. IL-18BP polypeptides, and DNA encoding
CC them, can be used to treat conditions requiring the protein
CC (claimed). Conditions include autoimmune diseases, type I diabetes,
CC rheumatoid arthritis, graft rejections, inflammatory bowel disease,
CC sepsis, multiple sclerosis, ischemic heart diseases, ischemic brain
CC injury, chronic hepatitis, psoriasis, and chronic/acute
CC pancreatitis. IL-18BP is also useful for purifying IL-18 (claimed).
XX
XX Sequence 161 AA:
SQ
Query Match 59.1%; Score 97; DB 20; Length 161;
Best Local Similarity 100.0%; Pred. No. 4e-90;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
AAW98005
ID AAW98005 standard; Protein, 113 AA.
XX
XX AAW98005;
AC
XX 21-JUN-1999 (first entry)
XX
XX Human interleukin-18 binding protein splice variant IL-18BPd.
DE
XX Interleukin-18 binding protein; IL-18BP; IL-18BPd; splice variant;
KW human; autoimmune disease; inflammation; diabetes; pancreatitis;
KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
KW psoriasis; inflammatory bowel disease; multiple sclerosis;
XX ischemic heart disease; ischemic brain injury; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..28
FT /note= "signal peptide"
FT Protein 29..113
FT /note= "mature protein"
XX
XX WO9909063-A1.
XX
XX 25-FEB-1999.
XX
XX 13-AUG-1998; 98WO-IL00379.
XX
XX 22-JUL-1998; 98IL-0125463.
XX 14-AUG-1997; 97IL-0121554.
XX 27-AUG-1997; 97IL-0121639.
XX 29-SEP-1997; 97IL-0121860.
XX 06-NOV-1997; 97IL-0122134.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX DiNarello C, Kim SH, Novick D, Rubinstein M;
PI WPI: 1999-180975/15.
XX N-PSDB; AAX24750.
XX
XX New interleukin-18 binding protein - useful for treating human
PT diseases, including autoimmune disease and inflammation
PT
XX Claim 3; Page 55; 100pp: English.
XX
XX The present sequence represents a human interleukin-18 binding
CC protein (IL-18BP) splice variant designated IL-18BPd. This is one
CC four novel splice variants (see also AAW98004-07), all putative
CC soluble proteins, that are encoded by cDNA clones (see AAX24749-52)
CC detected following a screening of human peripheral blood monocyte,
CC Jurkat T-cell, peripheral blood mononuclear cell and spleen cell
CC cDNA libraries. IL-18BPd is a low abundance variant. IL-18BP
CC polypeptides capable of binding IL-18 and/or modulating and/or
CC blocking IL-18 activity are provided, as are methods for their
CC isolation and recombinant production, DNA vectors expressing them,
CC vectors useful for their expression in humans and other mammals,
CC and antibodies against them. IL-18BP polypeptides, and DNA encoding
CC them, can be used to treat conditions requiring the protein
CC (claimed). Conditions include autoimmune diseases, type I diabetes,
CC rheumatoid arthritis, graft rejections, inflammatory bowel disease,
CC sepsis, multiple sclerosis, ischemic heart diseases, ischemic brain
CC injury, chronic hepatitis, psoriasis, and chronic/acute
CC pancreatitis. IL-18BP is also useful for purifying IL-18 (claimed).
XX
XX Sequence 113 AA:
SQ
Query Match 29.3%; Score 48; DB 20; Length 113;

```

Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TPVSQTTAATASVRSSTKDCPSQPPVPAKQCPALVETWPEVEPL 48
XX
DB 29 tpsvqtltaatasvrsstkdcpsqppvfpaakqcpalevltwpevevpl 76

RESULT 9
AAW83984
ID AAW83984 standard; Protein; 47 AA.

XX AAW83984;

DT 28-JUL-2000 (first entry)

XX Human IL-18 binding protein C-terminus.

XX Immunosuppressant; Interleukin 18 binding protein; IL18-BP; human; mouse;
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease; rapid amplification of cDNA ends; RACE.

XX Homo sapiens.

PN WO000012555-A1.

PD 09-MAR-2000.

PF 18-NOV-1998; 98WO-JP05186.

PR 01-SEP-1998; 98UP-0247588.

PR 18-NOV-1998; 98UP-0327914.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Torigoe K, Tanai M, Kurimoto M;

DR WPI: 2000-237850/20.

DR N-PSDB: AAA11006.

PT Interleukin 18-binding protein with activity of regulating

PS physiological actions of interleukin 18, useful as regulator and drug

CC due to excess immune reaction - organ rejection and in treating diseases

CC Example 2; Page 62; 71pp; Japanese.

CC The invention relates to novel interleukin 18 (IL-18)-binding proteins

CC from humans or mice which act as regulators and drugs for sensitivity

CC diseases and organ rejection and in treating diseases due to excess

CC immune reaction, e.g. in slowing down rejection after organ transplant,

CC and in treating autoimmune diseases. This sequence represents the

CC C-terminus of the interleukin 18 binding protein encoded by the 3' end

CC of the gene isolated by a 3' RACE (Rapid Amplification of cDNA Ends)

CC reaction.

XX Sequence 47 AA;

Query Match 28.7%; Score 47; DB 21; Length 47;
Best Local Similarity 100.0%; Pred. No. 5.8e-40;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 118 FSCVLDPPEOVORHVLQAGLRATLPTEALPSSHSPQOOG 164
XX
DB 1 fscvlvdppeqvgrhvlvqlaglratlpptealpsshspqpg 47

RESULT 10
AAW98008
ID AAW98008 standard; Peptide; 40 AA.
XX AAW98008;

XX 21-JUN-1999 (first entry)

DT Human interleukin-18 binding protein N-terminal peptide.

XX Interleukin-18 binding protein; IL-18BP; human; autoimmune disease;

XX inflammation; diabetes; pancreatitis; rheumatoid arthritis;

KW graft rejection; sepsis; chronic hepatitis; psoriasis;

KW inflammatory bowel disease; multiple sclerosis;

KW ischemic heart disease; ischemic brain injury; therapy.

XX Homo sapiens.

OS Key

FT Peptide

FT Protein

FT Location/Qualifiers

FT 1..28

FT /note="signal peptide"

FT 29..113

FT /note="mature protein"

PN WO9909063-A1.

PD 25-FEB-1999.

PF 13-AUG-1998; 98WO-IL00379.

PR 22-JUL-1998; 98IL-0125463.

PR 14-AUG-1997; 97IL-0121554.

PR 27-AUG-1997; 97IL-0121639.

PR 29-SEP-1997; 97IL-0121860.

PR 06-NOV-1997; 97IL-0122134.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Dinarello C, Kim SH, Novick D, Rubinstein M;

DR WPI: 1999-180975/15.

DR New interleukin-18 binding protein - useful for treating human

PT diseases, including autoimmune disease and inflammation

PS Claim 1; Page 63; 100pp; English.

CC This polypeptide comprises the 40 N-terminal amino acids of human

CC interleukin-18 binding protein (IL-18BP) mature polypeptide. The

CC same 40-amino acid sequence is found at the N-terminus of 4 novel

CC IL-18BP splice variants (see AAW98004-007). IL-18BP polypeptides,

CC including the splice variants, that are capable of binding IL-18

CC and/or modulating and/or blocking IL-18 activity are provided.

CC Methods for their isolation and recombinant production, DNA vectors

CC expressing them, vectors useful for their expression in humans and

CC other mammals, and antibodies against them are also provided.

CC IL-18BP polypeptides, and DNA encoding them, can be used to treat

CC conditions requiring the protein (claimed). Such conditions

CC include autoimmune diseases, type I diabetes, rheumatoid arthritis,

CC graft rejections, inflammatory bowel disease, sepsis, multiple

CC sclerosis, ischemic heart diseases, ischemic brain injury, chronic

CC hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is

CC also useful for purifying IL-18 (claimed).

XX Sequence 40 AA;

Query Match 24.4%; Score 40; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 6.2e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TPVSQTTAATASVRSSTKDCPSQPPVPAKQCPALVET 40
XX
DB 1 tpsvqtltaatasvrsstkdcpsqppvfpaakqcpalevt 40

RESULT 11
AA12716

ID AY12716 standard; Protein: 55 AA.
XX
AC AY12716;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human 5' EST secreted protein SEQ ID NO:306.
XX
KW Human: secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition.
XX
OS Homo sapiens.
XX
PN WO9906549-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-IB01231.
XX
PR 01-AUG-1997; 97US-0905279.
XX
PA (GEST) GENSET.
XX
PI Duclert A, Dumas Milne Edwards J, Lacroix B;
XX
DR WP1: 1999-153779/13.
DR N-PSDB: AAX51494.
XX
PT New nucleic acids encoding human secreted proteins - obtained from
PT cDNA libraries derived from testis, ovary, uterus and spleen tissue
XX
PS Claim 34: Page 404-405; 522pp; English.
XX
CC AAX51459 to AAX51691 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AY12681 to
CC AY12913, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell.
XX
SQ Sequence 55 AA:

Query Match 14.6%; Score 24; DB 20; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPVSGTTTAAATASVSRSTKDCPPSQ 24
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
Db 31 tpsqtltaataasvstskdpcpsq 54

RESULT 12
AAY83986
ID AAY83986 standard; Protein: 117 AA.
XX
AC AAY83986;
XX

DT 28-JUL-2000 (first entry)
XX
DE Mouse IL-18 binding protein 5' RACE fragment #1 encoded protein.
XX
KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease; rapid amplification of cDNA ends; RACE.
XX
OS Mus musculus.
XX
PN WO200012555-A1.
XX
PD 09-MAR-2000.
XX
PF 18-NOV-1998; 98WO-JP05186.
XX
PR 01-SEP-1998; 98JP-0247588.
PR 18-NOV-1998; 98JP-0327914.
XX
PA (HAYB) HAYASHIPARA SEIBUTSU KAGAKU.
XX
PI Torioge K, Tanai M, Kurimoto M;
XX
DR WP1: 2000-237850/20.
DR N-PSDB: AAA11008.
XX
PT Interleukin 18-binding protein with activity of regulating
PT physiological actions of interleukin 18, useful as regulator and drug
PT for sensitivity diseases and organ rejection and in treating diseases
PT due to excess immune reaction -
XX
PS Example 4: Page 65; 71pp; Japanese.
XX
CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC and in treating autoimmune diseases. This sequence represents the
CC protein encoded by the initial fragment isolated by a 5' RACE (Rapid
CC Amplification of cDNA Ends) reaction for the 5' end of the mouse
CC interleukin 12 binding protein coding sequence.
XX
SQ Sequence 117 AA:

Query Match 12.2%; Score 20; DB 21; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.1e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 FSILYWGNGSFIEHGRGL 84
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
Db 38 fslilywngsfiehlpgrl 57

RESULT 13
AAY83952
ID AAY83952 standard; Protein: 165 AA.
XX
AC AAY83952;
XX
DT 28-JUL-2000 (first entry)
XX
DE Mouse mature interleukin 18 binding protein.
XX
KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease.
XX
OS Mus musculus.
XX
PN WO200012555-A1.
XX
PD 09-MAR-2000.

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XX 18-NOV-1998; 98WO-JP05186.
PF 01-SEP-1998; 98JP-0247588.
PR 18-NOV-1998; 98JP-0327914.
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX Torigoe K, Taniai M, Kurimoto M;
XX WPI: 2000-237850/20.
DR N-PSDB; AAA11003.
XX
XX The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC and in treating autoimmune diseases. This sequence represents the mature
CC mouse interleukin 12 binding protein.
XX
SQ Sequence 165 AA;

```

```

Query Match 12.2%; Score 20; DB 21; Length 165;
Best Local Similarity 100.0%; Pred. No. 4.3e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 65 FSILYWLGNCSFIEHLPGRL 84
Db 62 fslilywlgnsgfiehlpgrl 81

```

```

RESULT 14
AAV83989
ID AAV83989 standard; Protein; 193 AA.
XX
AC AAV83989;
XX
DT 28-JUL-2000 (first entry)
XX
DE Full length mouse interleukin 18 binding protein.
XX
KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..28
FT /label= signal_peptide
FT Protein 29..193
FT /label= "mature IL-18 binding protein"
XX
XX WO200012555-A1.
XX
XX 09-MAR-2000.
XX
XX 18-NOV-1998; 98WO-JP05186.
XX
XX 01-SEP-1998; 98JP-0247588.
XX 18-NOV-1998; 98JP-0327914.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX Torigoe K, Taniai M, Kurimoto M;
PI

```

```

XX WPI: 2000-237850/20.
DR N-PSDB; AAA11011.
XX
XX Interleukin 18-binding protein with activity of regulating
PT physiological actions of interleukin 18, useful as regulator and drug
PT for sensitivity diseases and organ rejection and in treating diseases
PT due to excess immune reaction -
XX
XX Example 4; Page 67-69; 71pp: Japanese.
XX
XX The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC and in treating autoimmune diseases. This sequence represents the full
CC length mouse interleukin 12 binding protein.
XX
SQ Sequence 193 AA;

```

```

Query Match 12.2%; Score 20; DB 21; Length 193;
Best Local Similarity 100.0%; Pred. No. 5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 65 FSILYWLGNCSFIEHLPGRL 84
Db 90 fslilywlgnsgfiehlpgrl 109

```

```

RESULT 15
AAV83983
ID AAV83983 standard; Protein; 49 AA.
XX
AC AAV83983;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human IL-18 binding protein N-terminus.
XX
KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease; rapid amplification of cDNA ends; RACE.
XX
XX Homo sapiens.
XX
XX WO200012555-A1.
XX
XX 09-MAR-2000.
XX
XX 18-NOV-1998; 98WO-JP05186.
XX
XX 01-SEP-1998; 98JP-0247588.
XX 18-NOV-1998; 98JP-0327914.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX Torigoe K, Taniai M, Kurimoto M;
XX WPI: 2000-237850/20.
XX N-PSDB; AAA11005.
XX
XX Interleukin 18-binding protein with activity of regulating
PT physiological actions of interleukin 18, useful as regulator and drug
PT for sensitivity diseases and organ rejection and in treating diseases
PT due to excess immune reaction -
XX
XX Example 2; Page 61-62; 71pp: Japanese.
XX
XX The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC

```


CC and in treating autoimmune diseases. This sequence represents the
CC N-terminus of the interleukin 18 binding protein encoded by the 5' end
CC of the gene isolated by a 5' RACE (Rapid Amplification of cDNA Ends)
CC reaction.

XX
SQ Sequence 49 AA;

Query Match 11.6%; Score 19; DB 21; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TPVSQTTAATASVRSRKD 19
|||||
Db 31 tpvsqtltaatasvrstkd 49

Search completed: October 9, 2002, 01:52:26
Job time: 5277 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2002, 00:42:39 ; Search time 61.98 Seconds
(without alignments)
457.747 Million cell updates/sec

Title: US-09-786-130-1

Perfect score: 164
Sequence: 1 TPVSQTTTAAATASVRSSTKDP.....TLPPQGEALPSSSSPQQQG 164

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPREMBL_19:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	164	100.0	184	4	Q9UNH2 homo sapien
2	164	100.0	194	4	Q9DBR7 homo sapien
3	97	59.1	161	4	Q9NZAG homo sapien
4	27	16.5	193	11	Q9JUN2 ratu
5	20	12.2	191	11	Q9ZOM9 mus musculu
6	20	12.2	192	11	Q9ZOM9 mus musculu
7	20	12.2	193	11	Q9ZOM9 mus musculu
8	19	11.6	218	11	Q9ZOM9 mus musculu
9	19	11.6	235	12	Q9ZOM9 mus musculu
10	15	9.1	99	11	Q9CV30 mus musculu
11	8	4.9	290	3	Q9USK4 schizosacch
12	8	4.9	421	4	Q9USK4 schizosacch
13	8	4.9	467	10	Q9USK4 schizosacch
14	8	4.9	505	10	Q9USK4 schizosacch
15	8	4.9	634	5	Q9VDD2 drosophila
16	8	4.9	647	5	Q9VDD2 drosophila

17	7	4.3	50	2	Q9R4R9 bacillus st
18	7	4.3	86	11	Q9JIV3 ratu
19	7	4.3	167	2	Q935Y1 synechococ
20	7	4.3	167	16	Q915S0 pseudomonas
21	7	4.3	207	16	Q9A1X3 streptococ
22	7	4.3	240	5	Q9VMA8 drosophila
23	7	4.3	246	16	Q9VMA8 drosophila
24	7	4.3	263	5	Q9VMA8 drosophila
25	7	4.3	310	16	Q9VMA8 drosophila
26	7	4.3	330	4	Q9VMA8 drosophila
27	7	4.3	339	17	Q9VMA8 drosophila
28	7	4.3	356	11	Q9VMA8 drosophila
29	7	4.3	366	5	Q9VMA8 drosophila
30	7	4.3	374	15	Q9VMA8 drosophila
31	7	4.3	385	11	Q9VMA8 drosophila
32	7	4.3	385	11	Q9VMA8 drosophila
33	7	4.3	401	2	Q9FAR4 streptococ
34	7	4.3	404	2	Q9FAR4 streptococ
35	7	4.3	415	16	Q9A1I0 streptococ
36	7	4.3	421	13	Q9IBD2 streptococ
37	7	4.3	421	13	Q9IBD2 streptococ
38	7	4.3	434	2	Q9H4U9 streptococ
39	7	4.3	500	4	Q9HAX4 streptococ
40	7	4.3	500	4	Q9HAX4 streptococ
41	7	4.3	500	4	Q9HAX4 streptococ
42	7	4.3	500	16	Q9HAX4 streptococ
43	7	4.3	502	2	Q9HAX4 streptococ
44	7	4.3	551	10	Q9HAX4 streptococ
45	7	4.3	554	3	Q9C101 schizosacch

ALIGNMENTS

RESULT	ID	Query Match	Score	Length	DB ID	Description
1	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
2	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
3	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
4	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
5	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
6	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
7	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
8	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
9	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
10	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
11	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
12	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
13	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
14	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
15	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
16	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
17	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
18	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
19	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
20	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
21	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
22	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
23	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
24	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
25	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
26	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
27	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
28	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
29	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
30	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
31	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
32	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
33	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
34	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
35	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
36	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
37	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
38	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
39	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
40	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
41	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
42	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
43	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
44	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien
45	Q9UNH2	100.0%	164	184	4	Q9UNH2 homo sapien

OY 121 VLVDPEQVVRHVLAQLWAGLRATLPPTQALPSSHSSPQOOG 164
 DB 141 VLVDPEQVVRHVLAQLWAGLRATLPPTQALPSSHSSPQOOG 184

RESULT 2

Q9UBR7 PRELIMINARY: PRT: 194 AA.
 AC Q9UBR7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE INTERLEUKIN-18 BINDING PROTEIN PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=99192308; PubMed=10094485;
 RA Aizawa Y., Akita K., Tanai M., Korigoe K., Mori T., Nishida Y.,
 RA Ushio S., Nakada Y., Tanimoto T., Ikegami H., Ikeda M., Kurimoto M.,
 RT "Cloning and expression of Interleukin-18 binding protein.";
 RL FEBS Lett. 445:338-342(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99263157; PubMed=10329540;
 RA Xiang Y., Moss B.,
 RT "Identification of human and mouse homologs of the M51L-53L-54L
 RT family of secreted glycoproteins encoded by the Molluscum contagiosum
 RT poxvirus.";
 RL Virology 257:297-302(1999).
 DR EMBL: AB019504; BAA76374.1; -;
 DR EMBL: AF122906; AADA1051.1; -;
 DR InterPro: IPR003006; I9_MHC.
 DR Pfam: PF00047; 19; 1.
 KM Signal.
 FT CHAIN 1 30 POTENTIAL.
 FT SIGNAL 1 194 INTERLEUKIN-18 BINDING PROTEIN.
 SO SEQUENCE 194 AA; 21099 MW; 5E520D6E46AFA843 CRC64;

Query Match 100.0%; Score 164; DB 4; Length 194;
 Best Local Similarity 100.0%; Pred. No. 1.3e-159;
 Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TPVSQTTAATASVSTKPCPSQPPVFPAAKQCPALVETWPEVPLNGTSLSCVACS 60
 DB 31 TPVSQTTAATASVSTKPCPSQPPVFPAAKQCPALVETWPEVPLNGTSLSCVACS 90
 OY 61 RPPNFSILYWLNGSFIEHLPGRLMEGSTRSRGSGTGOLCALVLEQTLPAHSTNFCSC 120
 DB 91 RPPNFSILYWLNGSFIEHLPGRLMEGSTRSRGSGTGOLCALVLEQTLPAHSTNFCSC 150
 OY 121 VLVDPEQVVRHVLAQLWAGLRATLPPTQALPSSHSSPQOOG 164
 DB 151 VLVDPEQVVRHVLAQLWAGLRATLPPTQALPSSHSSPQOOG 194

RESULT 3
 Q9NZA9 PRELIMINARY: PRT: 161 AA.
 AC Q9NZA9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 DE INTERLEUKIN-18 BINDING PROTEIN D.
 GN IL18BP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20122593; PubMed=10655506;
 RA Kim S.H., Eisenstein M., Reznikov L., Fantuzzi G., Novick D.,
 RA Rubinstein M., Dinaarello C.A.,
 RT "Structural requirements of six naturally occurring isoforms of the
 RT IL-18 binding protein to inhibit IL-18.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1190-1195(2000).
 DR EMBL: AF215907; AAF31697.1; -;
 SO SEQUENCE 161 AA; 17246 MW; 28A04CCD92F4833D CRC64;

Query Match 59.1%; Score 97; DB 4; Length 161;
 Best Local Similarity 100.0%; Pred. No. 3.8e-91;
 Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TPVSQTTAATASVSTKPCPSQPPVFPAAKQCPALVETWPEVPLNGTSLSCVACS 60
 DB 29 TPVSQTTAATASVSTKPCPSQPPVFPAAKQCPALVETWPEVPLNGTSLSCVACS 88
 OY 61 RPPNFSILYWLNGSFIEHLPGRLMEGSTRSRGSGTG 97
 DB 89 RPPNFSILYWLNGSFIEHLPGRLMEGSTRSRGSGTG 125

RESULT 4

Q9JLN2 PRELIMINARY: PRT: 193 AA.
 AC Q9JLN2;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 DE INTERLEUKIN 18 BINDING PROTEIN.
 GN IL18BP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LEWIS;
 RA Im S.H., Venkatesh N., Barchan D., Souroujon M.C., Fuchs S.,
 RT "Cloning and characterization of rat IL-18 binding protein.";
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF154569; AAF72102.1; -;
 SO SEQUENCE 193 AA; 21085 MW; BDB23D80E44844B0 CRC64;

Query Match 16.5%; Score 27; DB 11; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1.9e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 ACSRPPNFSILYWLNGSFIEHLPGRL 84
 DB 83 ACSRPPNFSILYWLNGSFIEHLPGRL 109

RESULT 5
 Q9ZOM9 PRELIMINARY: PRT: 191 AA.
 AC Q9ZOM9;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE INTERLEUKIN-18 BINDING PROTEIN D PRECURSOR.
 GN IGFBP OR IL18BP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99146382; PubMed=10023777;

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RA Novick D., Kim S.H., Fantuzzi G., Reznikov L.L., Dinarello C.A.,
RA Rubinstein M.;
RT "Interleukin-18 binding protein: a novel modulator of the Th1 cytokine
RT response.";
RL Immunity 10:127-136(1999).
DR EMBL; AF110803; AAD17194.1; -.
DR MGD; MGI:133800; Ig1fBP.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
KW Signal.
FT SIGNAL.
FT CHAIN
FT 27 191 POTENTIAL.
SQ SEQUENCE 191 AA; 21035 MW; B2F306A905116E5B CRC64;

Query Match 12.2%; Score 20; DB 11; Length 191;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 65 FSILYWLNGSFIEHLPGRL 84
DB 88 FSILYWLNGSFIEHLPGRL 107

RESULT 6
O920N0 PRELIMINARY; PRT; 192 AA.
AC O920N0;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTERLEUKIN-18 BINDING PROTEIN C PRECURSOR.
GN IG1FBP OR IL18BP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RE SEQUENCE FROM N.A.
RX MEDLINE=99146382; PubMed=10023777;
RA Novick D., Kim S.H., Fantuzzi G., Reznikov L.L., Dinarello C.A.,
RA Rubinstein M.;
RT "Interleukin-18 binding protein: a novel modulator of the Th1 cytokine
RT response.";
RL Immunity 10:127-136(1999).
DR EMBL; AF110802; AAD17193.1; -.
DR MGD; MGI:133800; Ig1fBP.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
KW Signal.
FT SIGNAL.
FT CHAIN
FT 27 192 POTENTIAL.
SQ SEQUENCE 192 AA; 21668 MW; D828CBD328607421 CRC64;

Query Match 12.2%; Score 20; DB 11; Length 192;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 65 FSILYWLNGSFIEHLPGRL 84
DB 88 FSILYWLNGSFIEHLPGRL 107

RESULT 7
O90UH2 PRELIMINARY; PRT; 193 AA.
AC O90UH2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTERLEUKIN-18 BINDING PROTEIN PRECURSOR (INTERFERON GAMMA INDUCING
DE FACTOR BINDING PROTEIN).
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GN IG1FBP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RE SEQUENCE FROM N.A.
RX STRAIN=CD-1;
RC MEDLINE=99192308; PubMed=10094485;
RA Aizawa Y., Akita K., Tanai M., Korigoe K., Mori T., Nishida Y.,
RA Ushio S., Nukada Y., Tanimoto T., Ikegami H., Ikeda M., Kurimoto M.;
RT "Cloning and expression of interleukin-18 binding protein.";
RN FEBS Lett. 445:338-342(1999).
[2]
RE SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RX MEDLINE=99263157; PubMed=10329540;
RA Xiang Y., Moss B.;
RT "Identification of human and mouse homologs of the MCS1L-53L-54L
RT family of secreted glycoproteins encoded by the molluscan contagiosum
RT poxvirus.";
RN Virology 257:297-302(1999).
[3]
RE SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE, EMBRYO, AND SMALL INTESTINE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Frieschmann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido T., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Bono H., Baldairelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamija M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzairelli J., Mombeerts P.,
RA Nordone P., Ring B., Rindwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AB019505; BAA76375.1; -.
DR EMBL; AF122907; AAD1052.1; -.
DR EMBL; AK009721; BAB26462.1; -.
DR EMBL; AK003370; BAB22744.1; -.
DR EMBL; AK008452; BAB25677.1; -.
DR MGD; MGI:133800; Ig1fBP.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
KW Signal.
FT SIGNAL.
FT CHAIN
FT 29 193 POTENTIAL.
SQ SEQUENCE 193 AA; 21257 MW; D7AD4B0AB07C8248 CRC64;

Query Match 12.2%; Score 20; DB 11; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 65 FSILYWLNGSFIEHLPGRL 84
DB 90 FSILYWLNGSFIEHLPGRL 109

RESULT 8
O91W13 PRELIMINARY; PRT; 218 AA.
AC O91W13;
```

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE INTERLEUKIN 18 BINDING PROTEIN.
 GN 0541.
 OS Molluscum contagiosum virus subtype 1 (MCV1).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Molluscipoxvirus.
 OX NCBI_TaxID=10280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MADRID 99;
 RX MEDLINE=20231932; PubMed=10769064;
 RA Smith V.P., Bryant N.A., Alcamal A.;
 RT "Ectromella, vaccinia and cowpox viruses encode secreted interleukin
 RT 18 binding proteins";
 RL J. Gen. Virol. 81:1223-1230(2000).
 DR EMBL, AJ271163; CAB89814.1; -
 SQ SEQUENCE 218 AA; 23853 MW; 3FPA9C24DD24E75 CRC64;

Query Match 11.6%; Score 19; DB 12; Length 218;
 Best Local Similarity 100.0%; Pred. No. 3.3e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 HSTNFCVLVDEQVYVORH 132
 DB 113 HSTNFCVLVDEQVYVORH 131

RESULT 9
 ID Q98222 PRELIMINARY; PRT; 235 AA.
 AC Q98222;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE MC054L.
 GN MC054L.
 OS Molluscum contagiosum virus subtype 1 (MCV1).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Molluscipoxvirus.
 OX NCBI_TaxID=10280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96325459; PubMed=8670425;
 RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
 RA Moss B.;
 RT "Genome sequence of a human tumorigenic poxvirus: Prediction of
 RT specific host response-evasion genes.";
 RL Science 273:813-816(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
 RA Moss B.;
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL; U60315; AAC55182.1; -
 SQ SEQUENCE 235 AA; 25209 MW; BA47745C6860889 CRC64;

Query Match 11.6%; Score 19; DB 12; Length 235;
 Best Local Similarity 100.0%; Pred. No. 3.5e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 HSTNFCVLVDEQVYVORH 132
 DB 113 HSTNFCVLVDEQVYVORH 131

RESULT 10
 ID Q9CV30 PRELIMINARY; PRT; 99 AA.
 AC Q9CV30;
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE MC054L.
 GN MC054L.
 OS Molluscum contagiosum virus subtype 1 (MCV1).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Molluscipoxvirus.
 OX NCBI_TaxID=10280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MADRID 99;
 RX MEDLINE=20231932; PubMed=10769064;
 RA Smith V.P., Bryant N.A., Alcamal A.;
 RT "Ectromella, vaccinia and cowpox viruses encode secreted interleukin
 RT 18 binding proteins";
 RL J. Gen. Virol. 81:1223-1230(2000).
 DR EMBL, AJ271163; CAB89814.1; -
 SQ SEQUENCE 218 AA; 23853 MW; 3FPA9C24DD24E75 CRC64;

DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE INTERFERON GAMMA INDUCING FACTOR BINDING PROTEIN (FRAGMENT).
 GN IGFBP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TONGUE;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi Y., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., But C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohatsu S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL; AK009877; BAB26558.1; -
 DR MGD; MGI:1333800; Igfbp.
 FT NON-TER
 SQ SEQUENCE 99 AA; 10869 MW; 2CB08739D5DABE8C CRC64;

Query Match 9.1%; Score 15; DB 11; Length 99;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 70 WLNGSFIEHLPGR 84
 DB 1 WLNGSFIEHLPGR 15

RESULT 11
 ID Q9USK4 PRELIMINARY; PRT; 290 AA.
 AC Q9USK4;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE HYPOTHETICAL 32.6 KDA PROTEIN.
 GN SPC483.14.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972H-;
 RA Seeger K., Harris D., McDougall R.C., Rajandream M.A., Barrell B.G.;
 RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AL132870; CAB60688.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 290 AA; 32564 MW; 3FB1E295203EAD43 CRC64;

Query Match 4.9%; Score 8; DB 3; Length 290;

Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 PTOEALPS 155
Db 235 PTOEALPS 242

RESULT 12
015329

ID 015329 PRELIMINARY; PRT; 421 AA.

AC 015329;

DT 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE SECRETORY MUCIN MUC6 (FRAGMENT).

GN MUC6.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93194895; PubMed=7680650;

RA Toribara N.W., Robertson A.M., Ho S.B., Kuo W.L., Gum E., Hicks J.W.,

RA Gum J.R., Byrd J.C., Siddiki B., Kim Y.S.;

RT "Human gastric mucin. Identification of a unique species by expression

RT cloning.";

RL J. Biol. Chem. 268:5879-5885(1993).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=97341178; PubMed=9195947;

RA Toribara N.W., Ho S.B., Gum E., Gum J.R., Lau P., Kim Y.S.;

RT "The carboxyl-terminal sequence of the human secretory mucin, MUC6.

RT Analysis Of the primary amino acid sequence.";

RL J. Biol. Chem. 272:16398-16403(1997).

DR EMBL; U97698; AAC51370.1; -

DR InterPro: IPR000359; Cys_knot.

DR Pfam: PF00007; Cys_knot; 1.

DR SMART; SM00041; CT; 1.

DR PROSITE; PS01225; CTCK_2; 1.

FT NON_TER 1

SQ SEQUENCE 421 AA; 42717 MW; 90E319ED23A9F80 CRC64;

Query Match 4.9%; Score 8; DB 4; Length 421;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 PSSHSPQ 161

Db 128 PSSHSPQ 135

RESULT 13
004127

ID 004127 PRELIMINARY; PRT; 467 AA.

AC 004127;

DT 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE LETHAL LEAF-SPOT 1 (FRAGMENT).

GN LLS1.

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;

OC Panicoideae; Andropogoneae; Zea.

OX NCBI_TaxID=4577;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PA405 INRED LINE; TISSUE=LEAF;

RX MEDLINE=97248483; PubMed=9094711;

RA Gray J., Close P.S., Briggs S.P., Johal G.S.;

RT "A novel suppressor of cell death in plants encoded by the L1s1 gene

RT of maize.";

RL Cell 89:25-31(1997).

DR EMBL; U77345; AAC49676.1; -

DR InterPro: IPR001281; Rieske.

DR Pfam; PF00355; Rieske; 1.

FT NON_TER 1

SQ SEQUENCE 467 AA; 52661 MW; 2D298BA8F4B3B900 CRC64;

Query Match 4.9%; Score 8; DB 10; Length 467;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 PTOEALPS 155

Db 369 PTOEALPS 376

RESULT 14
004129

ID 004129 PRELIMINARY; PRT; 505 AA.

AC 004129;

DT 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE LETHAL LEAF-SPOT 1 (FRAGMENT).

GN LLS-1.

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;

OC Panicoideae; Andropogoneae; Zea.

OX NCBI_TaxID=4577;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=B73 INRED LINE;

RX MEDLINE=97248483; PubMed=9094711;

RA Gray J., Close P.S., Briggs S.P., Johal G.S.;

RT "A novel suppressor of cell death in plants encoded by the L1s1 gene

RT of maize.";

RL Cell 89:25-31(1997).

DR EMBL; U77346; AAC49678.1; -

DR InterPro: IPR001281; Rieske.

DR Pfam; PF00355; Rieske; 1.

FT NON_TER 505

SQ SEQUENCE 505 AA; 56302 MW; A464BA6F8F8FA9 CRC64;

Query Match 4.9%; Score 8; DB 10; Length 505;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 PTOEALPS 155

Db 422 PTOEALPS 429

RESULT 15
09VDD2

ID 09VDD2 PRELIMINARY; PRT; 634 AA.

AC 09VDD2;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE SNF4AGAMMA PROTEIN.

GN SNF4AGAMMA OR SNF4AGAMMA OR CG17299.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidae; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klimos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003733; AAF55864.1; -
 DR FlyBase: FBgn0025803; SNFAA-gamma.
 DR InterPro: IPR000644; CBS; 4.
 DR Pfam: PF00571; CBS; 4.
 DR SMART: SM00116; CBS; 4.
 SQ SEQUENCE 634 AA; 70174 MM; 3FFD0D53E54BBE7C CRC64;

Query Match 4.9%; Score 8; DB 5; Length 634;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 OTTTAATA 12
 |||||
 Db 544 OTTTAATA 551

Search completed: October 9, 2002, 01:53:45
 Job time: 4266 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2002, 01:47:19 ; Search time 19.28 Seconds
(without alignments)
329.357 Million cell updates/sec

Title: US-09-786-130-1
Perfect score: 164
Sequence: 1 TPVSOQTTRATASVSTKDP.....TLPPQGEALPSSHSPQDGS 164

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size: 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	84.8	197	118B_HUMAN	Q95998 homo sapien
2	8	4.9	368	RIBD_SYNY3	Q5158 s riboflavi
3	8	4.9	443	YAAU_ECOLI	P31679 escherichia
4	8	4.9	838	AXN2_RAT	Q70240 rattus norv
5	8	4.9	840	AXN2_MOUSE	Q88566 mus musculu
6	8	4.9	843	AXN2_HUMAN	Q9Y2E1 homo sapien
7	7	4.3	54	IOVO_CIRAE	P05579 citrus aenu
8	7	4.3	54	IOVO_OPHO	P52249 opisthocomu
9	7	4.3	125	PER_DROAN	Q03293 drosophila
10	7	4.3	353	HN3G_MOUSE	P35584 mus musculu
11	7	4.3	354	HN3G_RAT	P32183 rattus norv
12	7	4.3	401	AMPC_PSYIM	Q05455 psychobact
13	7	4.3	402	KAS2_STRCM	P41176 streptomyce
14	7	4.3	500	PTGI_HUMAN	Q16647 homo sapien
15	7	4.3	552	EFGL_CANAL	P43064 candida alb
16	7	4.3	600	DHSA_PARDE	Q59661 paracoccu
17	7	4.3	710	PAL2_ORYSA	P53443 oryza sativ
18	7	4.3	1017	HTRA_HUMAN	P54198 homo sapien
19	6	3.7	61	E306_ADB35	P17531 human adeno
20	6	3.7	65	MYHB_PIG	P81271 sus scrofa
21	6	3.7	79	RL11_DICDI	P61688 dictyostell
22	6	3.7	80	P8_RAT	Q54842 rattus norv
23	6	3.7	100	KV3C_HUMAN	P01621 homo sapien
24	6	3.7	108	GLRX_YEAST	P17685 saccharomyc
25	6	3.7	108	KV3A_HUMAN	P01619 homo sapien
26	6	3.7	109	KV3B_HUMAN	P01620 homo sapien
27	6	3.7	109	KV3D_HUMAN	P01622 homo sapien
28	6	3.7	109	KV3E_HUMAN	P01623 homo sapien
29	6	3.7	109	KV3G_HUMAN	P04206 homo sapien
30	6	3.7	116	CUDA_LOCOMI	P21789 locusta mig
31	6	3.7	118	DSR4_HUMAN	P56555 homo sapien
32	6	3.7	118	VE4_HPV13	Q02265 human papil
33	6	3.7	125	RL11_TOXCA	Q94793 toxocara ca

34	6	3.7	126	1	THN1_WHEAT	P01544 triticum ae
35	6	3.7	128	1	KV3K_HUMAN	P06311 homo sapien
36	6	3.7	129	1	KV3L_HUMAN	P18135 homo sapien
37	6	3.7	129	1	KV3M_HUMAN	P18136 homo sapien
38	6	3.7	136	1	SR14_HUMAN	P37108 homo sapien
39	6	3.7	136	1	H2B1_CHLRE	P05065 chlamydomon
40	6	3.7	153	1	Y805_AQUAE	O66989 aquilex aeo
41	6	3.7	155	1	UREE_KLEAE	P18317 klebsiella
42	6	3.7	158	1	UREE_KLEAE	P27691 bacteroides
43	6	3.7	160	1	FMA7_BACNO	P21664 felis silve
44	6	3.7	163	1	LACA_FELCA	P29205 sus scrofa
45	6	3.7	170	1	RL11_CHLRE	P50881 chlamydomon

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	197 AA.
ID	118B_HUMAN			
AC	095998; 096027; 095993;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-18 binding protein precursor (IL-18BP).			
GN	IL18BP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99146382; Pubmed=10023777;			
RA	Novick D., Kim S.-H., Fantuzzi G., Reznikov L.L., Dinarello C.A.,			
RA	Rubinstein M.;			
RT	"Interleukin-18 binding protein: a novel modulator of the Th1 cytokine			
RT	response.";			
RL	Immunity 10:127-136(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99192308; Pubmed=10094485;			
RA	Alzawa Y., Akita K., Tanial M., Torigoe K., Mori T., Nishida Y.,			
RA	Ushio S., Nukada Y., Tanimoto T., Ikegami H., Ikeda M., Kurimoto M.;			
RT	"Cloning and expression of interleukin-18 binding protein.";			
RL	FEBS Lett. 445:338-342(1999).			
CC	-1- FUNCTION: FUNCTIONS AS AN INHIBITOR OF THE EARLY TH1 CYTOKINE			
CC	RESPONSE.			
CC	-1- SUBUNIT: BINDS TO IL-18.			
CC	-1- SUBCELLULAR LOCATION: Secreted (Potential).			
CC	-1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: A/IL-18BP, B/IL-18BPB AND C/IL-			
CC	18BPB (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.			
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
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CC	-----			
EMBL:	AF110798; AAD17187.1; -			
EMBL:	AF110798; AAD17188.1; -			
EMBL:	AF110798; AAD17189.1; -			
EMBL:	AF110799; AAD17190.1; -			
EMBL:	AF110800; AAD17191.1; -			
EMBL:	AF110801; AAD17192.1; -			
EMBL:	AF110813; -			
EMBL:	InterPro: IPR003006; Ig_MHC.			
EMBL:	Pfam: PF00047; Ig_1.			
EMBL:	Immunoglobulin domain; Glycoprotein; Signal; Alternative splicing.			
EMBL:	SIGNAL			
EMBL:	1			
EMBL:	28			
EMBL:	POTENTIAL.			

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FT CHAIN 29 197 INTERLEUKIN-18 BINDING PROTEIN.
FT DOMAIN 77 155 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 84 148 BY SIMILARITY.
FT CARBOHYD 92 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 168 197 VSPRGLQEOEELCEFHMGKGGLCOSSL -> AGLRATL
FT VARSPLIC 77 113 PPTOLSPSSSSSPQOQ (IN ISOFORM A).
FT VARSPLIC 77 113 NCTSLSCVACSRPRPSILYWGSGFIEHLPGSLM
FT VARSPLIC 77 113 SMABGNLAPHRRSPALQDPQOSTAAGLRISTGPAAOP (IN
FT VARSPLIC 77 113 ISOFORM B).
FT VARSPLIC 114 197 MISSING (IN ISOFORM B).
FT VARSPLIC 114 197 MISSING (IN ISOFORM B).
SQ SEQUENCE 197 AA; 21698 MW; FID626AB2B285E1 CRC64;

Query Match 84.8%; Score 139; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.4e-135;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TPVSQTTATATASVSTKPCPSOPVPPAAKCPALAEVTEVEVPLNGTSLSCVACS 60
DB 29 TPVSQTTATATASVSTKPCPSOPVPPAAKCPALAEVTEVEVPLNGTSLSCVACS 88
OY 61 RPNPFSILYWLNGSGFIEHLPGRLWEGSTRERGSTGTQLCAKALVLEQLTPALHSTNFSC 120
DB 89 RPNPFSILYWLNGSGFIEHLPGRLWEGSTRERGSTGTQLCAKALVLEQLTPALHSTNFSC 148
OY 121 VLVDEPQVQVRHVLAQLM 139
DB 149 VLVDEPQVQVRHVLAQLM 167

RESULT 2
RIBD_SYNY3 STANDARD: PRT; 368 AA.
AC 055158;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Riboflavin biosynthesis protein ribd [includes:
DE diaminohydroxyphosphoribosylaminoimidazole deaminase (EC 3.5.4.26)
DE (Riboflavin-specific deaminase); 5-amino-6-(5-
DE phosphoribosylamino)uracil reductase (EC 1.1.1.193) (HTP reductase)].
OS RIBD OR SLR0066.
OC Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneke T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugitara M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
CC -1- FUNCTION: CONVERTS 2,5-DIAMINO-6-(RIBOSYLAMINO)-4(3H)-PYRIMIDINONE
CC 5'-PHOSPHATE INTO 5-AMINO-6-(RIBOSYLAMINO)-2,4(1H,3H)-
CC PYRIMIDINEDIONE 5'-PHOSPHATE.
CC -1- CATALYTIC ACTIVITY: 2,5-diamino-6-hydroxy-4-(5-
CC phosphoribosylamino)pyrimidine + H(2)O = 5-amino-6-(5-
CC phosphoribosylamino)uracil + NH(3).
CC -1- CATALYTIC ACTIVITY: 5-amino-6-(5-phosphoribitylamino)uracil +
CC NADP(+) = 5-amino-6-(5-phosphoribosylamino)uracil + NADPH.
CC -1- COFACTOR: ZINC (BY SIMILARITY).
CC -1- PATHWAY: SECOND AN THIRD STEPS OF RIBOFLAVIN BIOSYNTHESIS.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTIDINE AND
CC DEOXYCYTIDYLATE DEAMINASES FAMILY.
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE HTP
CC REDUCTASE FAMILY.
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CC -----
CC EMBL: D64001; BAA10295.1; -.
CC InterPro: IPR002734; RibD_C.
CC DR pfam: PF00383; dCMP_CytL_deam.
CC DR pfam: PF01872; RibD_C; 1.
CC DR PROSITE: PS00903; CYT_DCMP_DEAMINASES; 1.
CC KW Riboflavin biosynthesis; Hydroxylase; Zinc; Oxidoreductase; NADP;
CC Multifunctional enzyme; Complete proteome.
CC FT DOMAIN 1 146 DEAMINASE.
CC FT DOMAIN 147 368 REDUCTASE.
CC FT METAL 51 51 ZINC (BY SIMILARITY).
CC FT METAL 76 76 ZINC (BY SIMILARITY).
CC FT METAL 85 85 ZINC (BY SIMILARITY).
SQ SEQUENCE 368 AA; 39995 MW; BCDA8ED0916B50BC CRC64;

Query Match 4.9%; Score 8; DB 1; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 LVLEQLTP 111
DB 264 LVLEQLTP 271

RESULT 3
YAUU_ECOLI STANDARD: PRT; 443 AA.
AC P31679; P31578; P75628;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hypothetical metabolite transport protein yauu.
GN YAUU OR B0045.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92334977; PubMed=1630901;
RA Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
RA Isono K., Mizobuchi K., Nakata A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of
RT the 0-2.4 min region.";
RL Nucleic Acids Res. 20:3305-3308(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS
CC IN POSITION 142 AND 232 THAT PRODUCE TWO SEPARATE ORFS.
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 CC -----
 DR EMBL: D10483; BAA01321.1; ALT_FRAME.
 DR EMBL: AE000114; AAC73156.1; -.
 DR PIR: S40566; S40566.
 DR EcoGene: EG11566; yaau.
 DR InterPro: IPR003662; sub_transporter.
 DR Pfam: PF00083; sugar_tr; 1.
 DR PROSITE: PS00216; SUGAR_TRANSPORT_1; FALSE_NEG.
 DR PROSITE: PS00217; SUGAR_TRANSPORT_2; FALSE_NEG.
 KW Hypothetical protein; Transport; Transmembrane; Inner membrane;
 KW Complete proteome.
 FT DOMAIN 1 18 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 19 39 1 (POTENTIAL).
 FT DOMAIN 40 53 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 54 74 2 (POTENTIAL).
 FT DOMAIN 75 84 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 85 105 3 (POTENTIAL).
 FT DOMAIN 106 113 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 114 134 4 (POTENTIAL).
 FT DOMAIN 135 145 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 146 166 5 (POTENTIAL).
 FT DOMAIN 167 173 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 174 194 6 (POTENTIAL).
 FT DOMAIN 195 241 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 242 262 7 (POTENTIAL).
 FT DOMAIN 263 282 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 283 303 8 (POTENTIAL).
 FT DOMAIN 304 309 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 310 329 9 (POTENTIAL).
 FT DOMAIN 330 334 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 335 357 10 (POTENTIAL).
 FT DOMAIN 358 373 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 374 394 11 (POTENTIAL).
 FT DOMAIN 395 401 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 402 422 12 (POTENTIAL).
 FT DOMAIN 423 443 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 443 48666 MM; AEF484DB8109DE05 CRC64;
 SO SEQUENCE

Query Match 4.9%; Score 8; DB 1; Length 443;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 106 LEOLTPAL 113
 Db 41 LEOLTPAL 48

RESULT 4
 ID AXN2_RAT STANDARD; PRT; 838 AA.
 AC 070240;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Axin 2 (axis inhibition protein 2) (Conductin) (Axin-like protein)
 DE (Axin1).
 GN AXIN2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98226558; PubMed=9566905;
 RA Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M.,
 RA Kikuchi A.;
 RT "Axin, a member of the Axin family, interacts with both glycogen
 RT synthase kinase 3beta and beta-catenin and inhibits axis formation of
 RT Xenopus embryos.";
 RL Mol. Cell. Biol. 18:2867-2875(1998).
 CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN-REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
 CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
 CC OCCURS VIA THE ARMDILLO REPEATS CONTAINED IN BETA-CATENIN.
 CC TERNARY COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG AND THYMUS.
 CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A.
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
 CC -----
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 CC -----
 DR EMBL: AF017757; AAC40089.1; -.
 DR HSSP: P49799; IAGR.
 DR InterPro: IPR001158; DIX.
 DR InterPro: IPR000342; RGS.
 DR Pfam: PF00778; DIX; 1.
 DR Pfam: PF00615; RGS; 1.
 DR ProDom: PD001580; RGS; 1.
 DR ProDom: PD003639; DIX; 1.
 DR SMART: SM00021; DAX; 1.
 DR SMART: SM00315; RGS; 1.
 DR PROSITE: PS50132; RGS; 1.
 KW Developmental protein; Phosphorylation.
 FT DOMAIN 81 200 RGS-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 327 413 BETA-CATENIN BINDING SITE (BY
 FT DOMAIN 413 476 SIMILARITY).
 FT TRANSMEM 469 474 POLY-HIS.
 FT DOMAIN 756 838 DIX.
 SO SEQUENCE 838 AA; 92947 MM; 45B825C13BA07F37 CRC64;

Query Match 4.9%; Score 8; DB 1; Length 838;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 ATASVRS 17
 Db 257 ATASVRS 264

RESULT 5
 ID AXN2_MOUSE STANDARD; PRT; 840 AA.
 AC 088566; 090XJ6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Axin 2 (axis inhibition protein 2) (Conductin) (Axin-like protein)
 DE (Axin1).
 GN AXIN2.
 OS Mus musculus (Mus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98221239; PubMed-9554852;
 RA Behrens J., Jerchow B.-A., Wuertele M., Grimm J., Asbrand C.,
 RA Wirtz R., Kuehl M., Wedlich D., Birchmeier W.;
 RT "Functional interaction of an axin homolog, conductin, with beta-
 RT catenin, APC, and GSK3beta.";
 RL Science 280:596-599(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
 RA Jenkins N.A., Warburton D., Costantini F.;
 RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
 RT expression pattern, interaction with Axin and effects on embryonic
 RT axis formation.";
 RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
 CC -i FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN-REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
 CC -i SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
 CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
 CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
 CC TERNARY COMPLEX (BY SIMILARITY).
 CC -i SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -i PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A (BY SIMILARITY).
 CC -i SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -i SIMILARITY: CONTAINS 1 DIX DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF073788; AAC26047.1; -;
 DR EMBL: AF205889; AAF22800.1; -;
 DR HSSP: P49799; IAGR.
 DR MGD: MGI:1270862; Axin2.
 DR InterPro: IPR001158; DIX.
 DR InterPro: IPR000342; RGS.
 DR Pfam: PF00778; DIX; 1.
 DR Pfam: PF00615; RGS; 1.
 DR PRINTS: PR01301; RGS-PROTEIN.
 DR PRODOM: PD001580; RGS; 1.
 DR ProDom: PD003639; DIX; 1.
 DR SMART: SM00021; DAX; 1.
 DR SMART: SM00315; RGS; 1.
 DR PROSITE: PS50132; RGS; 1.
 DR Anti-oncogene; Phosphorylation.
 KW DOMAIN 81 200 GSK-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 327 413 BETA-CATENIN BINDING SITE (BY
 FT DOMAIN 413 478 SIMILARITY).
 FT POLY-HIS.
 FT DOMAIN 469 476 DIX.
 FT DOMAIN 758 840 DIX.
 FT CONFLICT 101 101 R -> K (IN REF. 2).
 FT CONFLICT 474 474 H -> Y (IN REF. 2).
 FT CONFLICT 484 484 S -> P (IN REF. 2).
 FT CONFLICT 503 503 F -> S (IN REF. 2).
 FT CONFLICT 603 603 G -> A (IN REF. 2).
 SO SEQUENCE 840 AA: 92934 MW: A07D5FE825DE7277 CRC64;

Query Match 4.9%; Score 8; DB 1; Length 840;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 ATASVST 17
 |||||
 DB 257 ATASVST 264
 RESULT 6
 AXIN2_HUMAN
 ID AXIN2_HUMAN STANDARD; PRT; 843 AA.
 AC O9Y2T1: O9Y84;
 DT 16-OCT-2001 (rel. 40, Created)
 DT 16-OCT-2001 (rel. 40, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Axin 2 (Axin inhibition protein 2) (conductin) (Axin-like protein)
 DE (Ax11).
 GN AXIN2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99168905; PubMed-10049590;
 RA Mai W., Qian C., Yokomizo A., Smith D.I., Liu W.;
 RT "Cloning of the human homolog of conductin (AXIN2), a gene mapping to
 RL chromosome 17q23-q24.";
 RL Genomics 55:341-344(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Lymphoblast;
 RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
 RA Jenkins N.A., Warburton D., Costantini F.;
 RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
 RT expression pattern, interaction with Axin and effects on embryonic
 RT axis formation.";
 RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
 CC -i FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN-REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
 CC -i SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
 CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
 CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
 CC TERNARY COMPLEX (BY SIMILARITY).
 CC -i SUBCELLULAR LOCATION: Cytoplasmic.
 CC -i TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND LYMPHOBLAST.
 CC -i PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A (BY SIMILARITY).
 CC -i SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -i SIMILARITY: CONTAINS 1 DIX DOMAIN.
 CC -----
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 CC -----
 DR EMBL: AF078165; AAD20976.1; -;
 DR EMBL: AF205888; AAF22799.1; -;
 DR HSSP: P49799; IAGR.
 DR MIM: 604025; -;
 DR InterPro: IPR001158; DIX.
 DR InterPro: IPR000342; RGS.
 DR Pfam: PF00778; DIX; 1.
 DR Pfam: PF00615; RGS; 1.
 DR PRINTS: PR01301; RGS-PROTEIN.
 DR PRODOM: PD001580; RGS; 1.
 DR ProDom: PD003639; DIX; 1.
 DR SMART: SM00021; DAX; 1.
 DR SMART: SM00315; RGS; 1.
 DR PROSITE: PS50132; RGS; 1.
 DR Developmental protein; Phosphorylation.
 KW

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FT DOMAIN 81 200 RGS.
FT DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 413 476 BETA-CATENIN BINDING SITE (BY
FT DOMAIN 469 474 SIMILARITY).
FT DOMAIN 761 843 POLY-HIS.
FT CONFLICT 37 62 DIX.
FT CONFLICT 346 346 O -> R (IN REF. 2).
FT CONFLICT 572 636 MISSING (IN REF. 2).
FT CONFLICT 687 687 P -> S (IN REF. 2).
FT CONFLICT 696 696 Q -> H (IN REF. 2).
SQ SEQUENCE 843 AA; 93557 MW; F7B62BED6AB464D CRC64;

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Query Match 4.9%; Score 8; DB 1; Length 843;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 10 ATASVRSF 17
Db 257 ATASVRSF 264

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RESULT 7
ID IOVO_CIRAE STANDARD; PRT: 54 AA.
AC P05579;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Ovomucoid (Fragment).
OS Circus aeruginosus (Marsh harrier).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Falconiformes; Accipitridae;
OC Accipitridae; Circus.
OX NCBI_TaxID=8964;
RN [1]
RP SEQUENCE.
RX MEDLINE=87157615; PubMed=3828298;
RA Laskowski M. Jr., Kato I., Ardelt W., Cook J., Denton A., Emple M.W.,
RA Kohr W.J., Park S.J., Parks K., Schatzley B.L., Schoenberger O.L.,
RA Tashiro M., Vichot G., Whalley H.E., Wiczkorek A., Wiczkorek M.;
RT "Ovomucoid third domains from 100 avian species: isolation,
RT sequences, and hypervariability of enzyme-inhibitor contact
RT residues."
RL Biochemistry 26:202-221(1987).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: AVIAN OVOMUCOID CONSIST OF THREE HOMOLOGOUS, TANDEM KAZAL
CC FAMILY INHIBITORY DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
CC PIR: B31443; B31443.
DR HSSP: P05586; 4OVO.
DR InterPro: IPR002350; Kazal.
DR Pfam: PF00050; Kazal; 1.
DR SMART: SM00280; KAZAL; 1.
DR PROSITE: PS00282; KAZAL; 1.
KW Serine protease inhibitor; Glycoprotein; Repeat; Egg white.
FT NON_TER 1 1
FT DOMAIN 4 54 KAZAL-LIKE 3.
FT ACT_SITE 16 17 REACTIVE BOND 3.
FT DISULFID 14 33
FT DISULFID 22 34
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .).
FT NON_TER 54 54
SQ SEQUENCE 54 AA; 5876 MW; 416C5E9A6DEBF3AD1 CRC64;

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Query Match 4.3%; Score 7; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 49 NGTSLIS 55
Db 43 NGTSLIS 49

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RESULT 8
ID IOVO_OPIHO STANDARD; PRT: 54 AA.
AC P52248;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Ovomucoid (Fragment).
OS Opisthocomus hoazin (Hoatzin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Opisthocomiformes; Opisthocomidae;
OC Opisthocomus.
OX NCBI_TaxID=30419;
RN [1]
RP SEQUENCE.
RX MEDLINE=94072078; PubMed=8251062;
RA Apostol I., Giletto A., Komiya T., Zhang W., Laskowski M. Jr.;
RT "Amino acid sequences of ovomucoid third domains from 27 additional
RT species of birds."
RL J. Protein Chem. 12:419-433(1993).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: AVIAN OVOMUCOID CONSIST OF THREE HOMOLOGOUS, TANDEM KAZAL
CC FAMILY INHIBITORY DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
CC HSSP: P05586; 4OVO.
DR InterPro: IPR002350; Kazal.
DR Pfam: PF00050; Kazal; 1.
DR SMART: SM00280; KAZAL; 1.
DR PROSITE: PS00282; KAZAL; 1.
KW Serine protease inhibitor; Glycoprotein; Repeat; Egg white.
FT NON_TER 1 1
FT DOMAIN 4 54 KAZAL-LIKE 3.
FT ACT_SITE 16 17 REACTIVE BOND 3.
FT DISULFID 14 33
FT DISULFID 22 34
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .).
FT NON_TER 54 54
SQ SEQUENCE 54 AA; 5828 MW; 95B10804D446583D CRC64;

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Query Match 4.3%; Score 7; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 49 NGTSLIS 55
Db 43 NGTSLIS 49

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RESULT 9
ID PER_DROAN STANDARD; PRT: 125 AA.
AC 003293;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Period circadian protein (Fragment).
GN PER.
OS Drosophila ananassae (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7217;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93196482; PubMed=8450754;
RA Pelxoto A.A., Campesan S., Costa R.H., Kyriacou C.P.;

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RT "Molecular evolution of a repetitive region within the per gene of
RT Drosophila."
RL Mol. Biol. Evol. 10:127-139(1993).
CC -1- FUNCTION: ESSENTIAL FOR BIOLOGICAL CLOCK FUNCTIONS. DETERMINES THE
CC PERIOD LENGTH OF CIRCADIAN AND ULTRADIAN RHYTHMS: AN INCREASE IN
CC PER DOSAGE LEADS TO SHORTENED CIRCADIAN RHYTHMS AND A DECREASE
CC LEADS TO LENGTHENED CIRCADIAN RHYTHMS. ESSENTIAL FOR THE CIRCADIAN
CC RHYTHMICITY OF LOCOMOTOR ACTIVITY, ECLOSION BEHAVIOR, AND FOR THE
CC RHYTHMIC COMPONENT OF THE MALE COURTSHIP SONG THAT ORIGINATES IN
CC THE THORACIC NERVOUS SYSTEM. THE BIOLOGICAL CYCLE DEPENDS ON THE
CC RHYTHMIC FORMATION AND NUCLEAR LOCALIZATION OF THE TIM-PER
CC COMPLEX. LIGHT INDUCES THE DEGRADATION OF TIM, WHICH PROMOTES
CC ELIMINATION OF PER. NUCLEAR ACTIVITY OF THE HETERODIMER
CC COORDINATIVELY REGULATES PER AND TIM TRANSCRIPTION THROUGH A
CC NEGATIVE FEEDBACK LOOP. BEHAVES AS A NEGATIVE ELEMENT IN CIRCADIAN
CC TRANSCRIPTIONAL LOOP. DOES NOT APPEAR TO BIND DNA, SUGGESTING
CC INDIRECT TRANSCRIPTIONAL INHIBITION (BY SIMILARITY).
CC -1- SUBUNIT: FORMS HETERODIMER WITH TIMELESS (TIM); THE COMPLEX THEN
CC TRANSLOCATES INTO THE NUCLEUS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR AT SPECIFIC PERIODS OF THE DAY.
CC FIRST ACCUMULATES IN THE PERINUCLEAR REGION ABOUT ONE HOUR BEFORE
CC TRANSLLOCATION INTO THE NUCLEUS. INTERACTION WITH TIM IS REQUIRED
CC FOR NUCLEAR LOCALIZATION (BY SIMILARITY).
CC -1- DOMAIN: THE RUN OF GLY-THR IS IMPLICATED IN THE MAINTENANCE OF
CC CIRCADIAN PERIOD AT DIFFERENT TEMPERATURES. DELETION OF THE REPEAT
CC LEADS TO A SHORTENING OF THE COURSHIP SONG CYCLE PERIOD, AND THUS
CC COULD BE IMPORTANT FOR DETERMINING FEATURES OF SPECIES-SPECIFIC
CC MATING BEHAVIOR (BY SIMILARITY).
CC -1- PTM: PHOSPHORYLATED WITH A CIRCADIAN RHYTHMICITY, PROBABLY BY THE
CC DOUBLE-TIME PROTEIN (DBT). PHOSPHORYLATION COULD BE IMPLICATED IN
CC THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER
CC PER-TIM (BY SIMILARITY).
CC -----
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CC -----
DR EMBL: L06335; AAA28758.1; -.
DR FLYBASE: FBgn0012142; DanaPer.
KW Biological rhythms; Repeat; Nuclear protein; Phosphorylation.
FT NON_TER 1 1
FT DOMAIN 30 77 G-T REPEATS.
FT DOMAIN 96 102 POLY-THR.
FT NON_TER 125 125
SQ SEQUENCE 125 AA; 11118 MW; C733DD3586458A6F CRC64;

Query Match 4.3%; Score 7; DB 1; Length 125;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 TTTAATA 12
DB 105 TTTAATA 111

RESULT 10
HN3G_MOUSE STANDARD; PRT; 353 AA.
AC P35584;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Hepatocyte nuclear factor 3-gamma (HNF-3G).
GN HNF3G OR FOXA3 OR TCF3G OR TCF-3G.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94307723; PubMed=8034310;
RA Kaetner K., Hiemisch H., Luckow B., Schuetz G.;
RT "The Hnf-3 gene family of transcription factors in mice: gene
RT structure, cDNA sequence, and mRNA distribution.";
RL Genomics 20:377-385(1994).
CC -1- FUNCTION: TRANSCRIPTION ACTIVATOR FOR A NUMBER OF LIVER GENES
CC SUCH AS AFP, ALBUMIN, TYROSINE AMINOTRANSFERASE, PEPC, ETC.
CC INTERACTS WITH THE CIS-ACTING REGULATORY REGIONS OF THESE GENES.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: RESTRICTED MAINLY TO ENDODERM-DERIVED TISSUES
CC (LUNG, LIVER, STOMACH, AND SMALL INTESTINE), ALSO PRESENT
CC ADDITIONALLY IN OVARY, TESTIS, HEART, AND ADIPOSE TISSUE, BUT
CC MISSING FROM LUNG.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION PEAKS AROUND DAY 15.5 OF
CC GESTATION.
CC -----
CC -1- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
CC -----
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CC -----
DR EMBL: X74938; CAA52892.1; -.
DR PIR: S37186; S37186.
DR HSSP: 063245; 2HFH.
DR TRANSFAC: T02345; -.
DR MGD: MGI:1347477; Foxa3.
DR InterPro: IPR001766; Fork head.
DR Pfam: PF00250; Fork head; 1.
DR PRINTS: PR00053; FORKHEAD.
DR SMART: SM00339; FH; 1.
DR PROSITE: PS00657; FORK_HEAD_1; 1.
DR PROSITE: PS00658; FORK_HEAD_2; 1.
DR PROSITE: PS50039; FORK_HEAD_3; 1.
DR DNA-binding: Nuclear protein; Transcription regulation; Activator.
FT DNA_BIND 118 209
FT SEQUENCE 353 AA; 37601 MW; 28F060A8B944D5B9 CRC64;

Query Match 4.3%; Score 7; DB 1; Length 353;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 TTTAATA 12
DB 243 TTTAATA 249

RESULT 11
HN3G_RAT STANDARD; PRT; 354 AA.
AC P32183;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hepatocyte nuclear factor 3-gamma (HNF-3G).
GN HNF3G OR TCF3G OR TCF-3G.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91160974; PubMed=1672118;
RA Lai E., Prezioso V.R., Tao W.F., Chen W.S., Darnell J.E. Jr.;
RT "Hepatocyte nuclear factor 3 alpha belongs to a gene family in
RT mammals that is homologous to the Drosophila homeotic gene fork

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RT head.";
 RL Genes Dev. 5:416-427(1991).
 RN [2]
 RP STRUCTURE BY NMR OF 107-223.
 RX MEDLINE=93323996; PubMed=6332212;
 RA Clark K.L., Halsey E.D., Lai E., Burley S.K.;
 RT "o-crystal structure of the HNF-3/fork head DNA-recognition motif
 resembles histone H5".
 RL Nature 364:412-420(1993).
 CC -1- FUNCTION: TRANSCRIPTION ACTIVATOR FOR A NUMBER OF LIVER GENES
 CC SUCH AS AFP, ALBUMIN, TYROSINE AMINOTRANSFERASE, PEPCK, ETC.
 CC INTERACTS WITH THE CIS-ACTING REGULATORY REGIONS OF THESE GENES.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: Liver.
 CC -1- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
 CC -----
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 CC -----
 DR EMBL: L09648; AAA41339.1; -
 DR PIR: S35090; S35090.
 DR HSSP: Q63245; 2HRH.
 DR TRANSFAC: T01050; -
 DR InterPro: IPR001766; Fork_head.
 DR Pfam: PF00250; Fork_head; 1.
 DR PRINTS: PR00053; FORKHEAD.
 DR SMART: SM00339; FH; 1.
 DR PROSITE: PS00657; FORK_HEAD_1; 1.
 DR PROSITE: PS00658; FORK_HEAD_2; 1.
 DR PROSITE: PS50039; FORK_HEAD_3; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation; Activator.
 FT DNA BIND 118 209 FORK-HEAD.
 SQ SEQUENCE 354 AA; 37652 MW; 318B01EC6FC365C CRC64;

 Query Match 4.3%; Score 7; DB 1; Length 354;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 6 TTTAATA 12
 Db 243 TTTAATA 249

 RESULT 12
 AMPC_PSYIM STANDARD; PRT; 401 AA.
 ID AMPC_PSYIM
 AC 005465;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Beta-lactamase precursor (EC 3.5.2.6) (Cephalosporinase).
 GN AMPC OR BLA.
 OS Psychrobacter immobilis.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
 OC Psychrobacter.
 OX NCBI_TaxID=498;
 RN [1]
 RP SEQUENCE FROM N.A., SEQUENCE OF 40-47, AND CHARACTERIZATION.
 RX STRAIN=AS;
 RX MEDLINE=9217442; PubMed=9063463;
 RA Feller G., Zekhnin Z., Lamotte-Brasseur J., Gerday C.H.;
 RT "Enzymes from cold-adapted microorganisms. The class C beta-lactamase
 from the antarctic psychrophile Psychrobacter immobilis AS".
 RL Eur. J. Biochem. 244:186-191(1997).
 CC -1- FUNCTION: THIS PROTEIN IS A SERINE BETA-LACTAMASE WITH A SUBSTRATE
 CC SPECIFICITY FOR CEPHALOSPORINS.
 CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-

CC -1- amino acid.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE CLASS-C BETA-LACTAMASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X83586; CA58569.1; -
 DR HSSP: P05364; 2BLT.
 DR InterPro: IPR001466; Beta_Lactam.
 DR InterPro: IPR001586; Beta_Lactam_C.
 DR Pfam: PF00144; beta-lactamase; 2.
 DR PROSITE: PS00336; BETA-LACTAMASE_C; 1.
 KW Hydrolase; Antibiotic resistance; Signal.
 FT SIGNAL 1 39
 FT CHAIN 40 401 BETA-LACTAMASE.
 FT ACT_SITE 102 102 BY SIMILARITY.
 FT BINDING 353 355 SUBSTRATE (BY SIMILARITY).
 SQ SEQUENCE 401 AA; 44450 MW; 93F0DB278EA8E043 CRC64;

 Query Match 4.3%; Score 7; DB 1; Length 401;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 48 LNTLSTL 54
 Db 117 LNTLSTL 123

 RESULT 13
 KAS2_STRCM STANDARD; PRT; 402 AA.
 ID KAS2_STRCM
 AC P41176;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE putative polyketide beta-ketoacyl synthase 2 (EC 2.3.1.-) (ORF 2).
 OS Streptomyces cinnamonensis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1900;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3823.5;
 RX MEDLINE=92374994; PubMed=1508151;
 RA Arrowsmith T.J., Malpartida F., Sherman D.H., Birch A., Hopwood D.A.,
 RA Robinson J.A.;
 RT "Characterisation of acti-homologous DNA encoding polyketide synthase
 RT genes from the monensin producer Streptomyces cinnamonensis".
 RL Mol. Gen. Genet. 234:254-264(1992).
 CC -1- PATHWAY: BIOSYNTHESIS OF THE POLYKETIDE ANTIBIOTIC MONENSIN.
 CC -1- MISCELLANEOUS: THIS PUTATIVE KETOACYL SYNTHASE LACKS THE ACTIVE
 CC SITE CYSTEINE.
 CC -1- SIMILARITY: BELONGS TO THE BETA-KETOACYL-ACP SYNTHASES FAMILY.
 CC -----
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 CC -----
 DR EMBL: Z11511; CA477597.1; -
 DR PIR: S25077; S25077.
 DR InterPro: IPR000794; Ketoacyl-synt.
 DR Pfam: PF00109; ketoacyl-synt; 1.

DR Pfam: PF02801; ketoacyl-synt_C.1.
 SQ Antibiotic biosynthesis; Transferase; Acyltransferase.
 SEQUENCE 402 AA: 41270 MW: 348657D10201C214 CRC64;

Query Match 4.3%; Score 7; DB 1; Length 402;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 EHLPRRL 84
 |||||
 DB 59 EHLPRRL 65

RESULT 14
 ID PGTI_HUMAN STANDARD; PRT: 500 AA.
 AC 016647;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Prostacyclin synthase (EC 5.3.99.4) (Prostaglandin I2 synthase).
 GN PTGS OR CYP8 OR CYP8A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Arteria;
 RX MEDLINE=94242046; PubMed=8185632;
 RA Miyata A., Hara S., Yokoyama C., Inoue H., Ullrich V., Tanabe T.;
 RT "Molecular cloning and expression of human prostacyclin synthase.";
 RL Biochem. Biophys. Res. Commun. 200:1728-1734(1994).
 RN [2]
 RP SEQUENCE FROM N.A. AND VARIANTS LEU-38; ARG-118 AND SER-379.
 RX MEDLINE=21177061; PubMed=11281454;
 RA Chevalier D., Cauffiez C., Bernard C., Lo-Guidice J.-M., Allorge D.,
 RA Pazio F., Ferrari N., Libersa C., Lhermitte M., D'Halluin J.C.,
 RA Broly F.;
 RT "Characterization of new mutations in the coding sequence and
 5'-untranslated region of the human prostacyclin synthase gene
 (CYP8A1).";
 RL Hum. Genet. 108:148-155(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Delouis P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A.W., Laird G.K., Lawlor S.,
 RA Lehesvahto M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McElay K., McMurtry A.A.,
 RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).

CC - FUNCTION: CATALYZES THE ISOMERIZATION OF PROSTAGLANDIN H2 TO
 CC PROSTACYCLIN (= PROSTAGLANDIN I2).
 CC - CATALYTIC ACTIVITY: (5Z,13E)-(15S)-9- α ,11- α -epidioxo-15-
 CC hydroxyprosta-5,13-dienoate = (5Z,13E)-(15S)-6,9- α -epoxy-11-
 CC α ,15-dihydroxyprosta-5,13-dienoate.
 CC - SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM MEMBRANE. MAY BE
 CC ANCHORED TO THE MEMBRANE VIA A SINGLE TRANSMEMBRANE DOMAIN.
 CC - TISSUE SPECIFICITY: WIDELY EXPRESSED; PARTICULARLY ABUNDANT IN
 CC OVARY, HEART, SKELETAL MUSCLE, LUNG, AND PROSTATE.
 CC - SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 CC - DATABASE: NAME=cytochrome p450 Allele Nomenclature Committee;
 CC NOTE=CYP8A1 alleles;
 CC WWW="http://www.imm.ki.se/cypalleles/cyp8a1.htm".
 CC -----
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 CC -----
 DR EMBL: D38145; BAA07343.1; -;
 DR EMBL: AF287048; AAG31781.1; -;
 DR EMBL: AF287049; AAG31782.1; -;
 DR EMBL: AL118525; CAC14162.1; -;
 DR MIM: 601699; -;
 DR InterPro: IPR001128; Cyt_P450.
 DR Pfam: PF00067; P450; 2.
 DR PRINTS: PR00385; P450.
 DR PROSITE: PS00086; CYTOCHROME_P450, FALSE_NEG.
 KW Isomerase; Prostaglandin biosynthesis; Heme; Transmembrane;
 KW Endoplasmic reticulum; Polymorphism.
 FT BINDING 1 20 POTENTIAL.
 FT VARIANT 38 38 HEME (BY SIMILARITY).
 FT VARIANT 118 118 P->L (IN CYP8A1*2).
 FT VARIANT 118 118 S->R (IN CYP8A1*3).
 FT VARIANT 379 379 /FTid=VAR_010916.
 FT VARIANT 379 379 R->S (IN CYP8A1*4).
 FT /FTid=VAR_010917.
 SO SEQUENCE 500 AA: 57103 MW: 39595442BFC0B625 CRC64;
 Query Match 4.3%; Score 7; DB 1; Length 500;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 PYSQTTT 8
 |||||
 DB 323 PYSQTTT 329
 RESULT 15
 ID EFG1_CANAL STANDARD; PRT: 552 AA.
 AC P43064;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Enhanced filamentous growth protein.
 GN EFG1 OR EFG.
 OS Candida albicans (Yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10231;
 RX MEDLINE=97299875; PubMed=9155024;
 RA Stoldt V.R., Sonneborn A., Leuker C.E., Ernst J.F.;
 RT "Efg1p, an essential regulator of morphogenesis of the human pathogen
 Candida albicans, is a member of a conserved class of bHLH proteins


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RT  regulating morphogenetic processes in fungi."
RL  EMBL J. 16:1982-1991(1997).
CC  -I- FUNCTION: PUTATIVE TRANSCRIPTION FACTOR THAT STIMULATES
CC  PSEUDOHYPHAL MORPHOGENESIS.
CC  -I- SUBCELLULAR LOCATION: Nuclear (Potential).
CC  -I- SIMILARITY: BELONGS TO THE EFG1/PHD1/STU4 FAMILY.
CC  -----
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; Z32687; CAAB3640.1; -.
DR  InterPro; IPR003163; Yeast_DNA_bind.
DR  Pfam; PF02292; Yeast_DNA_bind; 1.
KW  Transcription regulation; Nuclear protein; DNA-binding.
FT  DOMAIN 34 37 POLY-GLN.
FT  DOMAIN 46 50 POLY-GLN.
FT  DOMAIN 83 93 POLY-GLN.
FT  DOMAIN 315 326 POLY-ALA.
FT  DOMAIN 332 338 POLY-PRO.
FT  DOMAIN 438 446 POLY-GLN.
FT  DOMAIN 470 473 POLY-GLN.
FT  DOMAIN 483 493 POLY-GLN.
FT  DOMAIN 496 499 POLY-GLN.
SQ  SEQUENCE 552 AA; 59964 MW; F94FD94FC2E06EB7 CRC64;

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Query Match          4.3%; Score 7; DB 1; Length 552;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  6 TTTAATA 12
    |||||
DB  343 TTTAATA 349

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Search completed: October 9, 2002, 02:52:57
 Job time: 3938 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 00:57:49 ; Search time 38.03 Seconds
(without alignments)
414.374 Million cell updates/sec

Title: US-09-786-130-1
Perfect score: 164
Sequence: 1 TPVSGTTTATATASVSTKDP.....TLPPQGEALPSSHSPPQOG 164

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: PIR-71:*

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	11.6	235	2 T30656	hypothetical prote
2	8	4.9	290	2 T50434	hypothetical prote
3	8	4.9	368	2 S74377	riboflavin biunct
4	8	4.9	443	2 E64725	yeau protein - Esc
5	8	4.9	443	2 H90634	probable transport
6	8	4.9	443	2 H85485	probable transport
7	8	4.9	520	2 T04136	cell death suppress
8	8	4.9	838	2 T08423	Axin homolog Axil
9	7	4.3	54	2 B31443	ovomucoid, third d
10	7	4.3	54	2 H61588	hypomucoid (PSTI-ty
11	7	4.3	147	2 T49624	hypothetical prote
12	7	4.3	176	2 F83531	hypothetical prote
13	7	4.3	246	2 C70527	hypothetical prote
14	7	4.3	310	2 A70421	fructose-1,6-bisph
15	7	4.3	330	2 S37595	mucin JUI10 - huma
16	7	4.3	339	2 A72609	probable deublockin
17	7	4.3	353	1 C54258	transcription fact
18	7	4.3	354	1 S35090	transcription fact
19	7	4.3	402	1 S25077	monensin polyketid
20	7	4.3	500	1 JC2231	prostaglandin-I sy
21	7	4.3	500	2 E83882	alpha-L-arabinofur
22	7	4.3	551	2 T01832	hypothetical prote
23	7	4.3	552	2 S49338	transcription fact
24	7	4.3	594	2 D97431	probable alpha-glu
25	7	4.3	600	2 T46880	succinate dehydrog
26	7	4.3	613	2 D97676	succinate dehydrog
27	7	4.3	613	2 AB2901	succinate dehydrog
28	7	4.3	630	2 AD3272	succinate dehydrog
29	7	4.3	702	2 A69140	ATP-dependent heli

30	7	4.3	710	2 S66313	phenylalanine ammo
31	7	4.3	766	2 S45344	Tup1 like enhancer
32	7	4.3	779	2 T21021	hypothetical prote
33	7	4.3	891	2 T29561	hypothetical prote
34	7	4.3	1017	2 I37465	HIRA protein - hum
35	7	4.3	1042	2 S76045	hypothetical prote
36	7	4.3	1069	2 S27922	nuclear antigen EB
37	7	4.3	1213	2 T51032	hypothetical prote
38	7	4.3	1348	2 S27812	probable epidermal
39	7	4.3	1348	2 A43917	probable epidermal
40	7	4.3	1388	2 T00063	hypothetical prote
41	7	4.3	1617	2 B86483	protein F5J5.15 (I
42	7	4.3	5126	2 S40450	ryanodine receptor
43	6	3.7	22	2 H30608	ig kappa chain V-I
44	6	3.7	26	2 G30608	ig kappa chain V-I
45	6	3.7	26	2 D30607	ig kappa chain V-I

ALIGNMENTS

RESULT 1
T30656
hypothetical protein 54L - Molluscum contagiosum virus 1
N:Alternate names: MC054L
C:Species: Molluscum contagiosum virus 1
C>Date: 05-Nov-1999 #sequence-revision 05-Nov-1999 #text-change 11-May-2000
C:Accession: T30656
R:Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host
A:Reference number: Z20876; MUID:96325459
A:Accession: T30656
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-235 <SEN>
A:Cross-references: EMBL:U60315; PIDN:AMC5182.1
C:Genetics:
A:Note: MC054L

Query Match 11.6%; Score 19; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 HSTNFCVLVDPEQVGRH 132
Db 113 HSTNFCVLVDPEQVGRH 131

RESULT 2
T50434
hypothetical protein SPCC4B3.14 [imported] - fission yeast (Schizosaccharomyces pombe
C:Species: Schizosaccharomyces pombe
C>Date: 09-Jun-2000 #sequence-revision 09-Jun-2000 #text-change 09-Jun-2000
C:Accession: T50434
R:Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, November 1999
A:Reference number: Z25033
A:Accession: T50434
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-290 <SEE>
A:Cross-references: EMBL:AL132870; PIDN:CAB60688.1; GSPDB:GN00068; SPDB:SPCC4B3.14
A:Experimental source: strain 972h(-); cosmid c4B3
C:Genetics:
A:Gene: SPDB:SPCC4B3.14
A:Map position: 3

Query Match 4.9%; Score 8; DB 2; Length 290;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 PROEALPS 155
 11111111
 DB 235 PROEALPS 242

RESULT 3

S74377
 riboflavin bifunctional biosynthesis protein ribG [similarity] - *Synechocystis* sp. (strain N.Altinate names: hypothetical protein slr0066; riboflavin-specific deaminase
 N.Contains: 5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193); diaminohyo
 C.Species: *Synechocystis* sp.
 A.Variety: FCC 6803
 C.Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000
 C.Accession: S74377
 R.Kanehko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A>Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
 s.

A.Reference number: S74322; MUID:97061201
 A.Accession: S74377

A>Status: nucleic acid sequence not shown; translation not shown

A.Molecule type: DNA

A.Residues: 1-368 <KAN>

A.Cross-references: EMBL:D64001; GB:AB001339; NID:q1001102; PIDN:BAA10295.1; PID:q100115
 A.Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C.Genetics:

A.Gene: ribG

C.Superfamily: Chlamydia pneumoniae riboflavin-specific deaminase

C.Keywords: hydrolase; oxidoreductase

Query Match 4.9%; Score 8; DB 2; Length 368;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 LVLEQLTP 111
 11111111
 DB 264 LVLEQLTP 271

RESULT 4
 E64725
 yaau protein - *Escherichia coli*

C.Species: *Escherichia coli*

C.Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 20-Jun-2000

C.Accession: E64725; S40566

R.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A>Title: The complete genome sequence of *Escherichia coli* K-12.

A.Reference number: A64720; MUID:97426617

A.Accession: E64725

A>Status: nucleic acid sequence not shown; translation not shown

A.Molecule type: DNA

A.Residues: 1-443 <BLAT>

A.Cross-references: GB:AE000114; GB:U00096; NID:q1786217; PIDN:AAC73156.1; PID:q1786229;
 A.Experimental source: strain K-12, substrain MG1655

R.Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isono, K.; Mizobu
 submitted to the EMBL Data Library, December 1992

A.Description: Systematic sequencing of the *Escherichia coli* genome: analysis of the 0-2

A.Reference number: S40531

A.Accession: S40566

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 'MKSSSRKPG', 233-239, 'C', 241-303, 'S', 305-394, 'D', 396-443 <YUR>

A.Cross-references: EMBL:D10483; NID:q216434; PIDN:BAA01321.1; PID:q216470

C.Genetics:

A.Gene: yaau

C.Superfamily: yaau protein

C.Keywords: transmembrane protein; transport protein

F:25-41/Domain: Transmembrane #status predicted <TM1>

F:57-73/Domain: transmembrane #status predicted <TM2>
 F:87-103/Domain: transmembrane #status predicted <TM3>
 F:106-122/Domain: transmembrane #status predicted <TM4>
 F:175-191/Domain: transmembrane #status predicted <TM5>
 F:244-260/Domain: transmembrane #status predicted <TM6>
 F:281-297/Domain: transmembrane #status predicted <TM7>
 F:313-329/Domain: transmembrane #status predicted <TM8>
 F:332-348/Domain: transmembrane #status predicted <TM9>
 F:369-385/Domain: transmembrane #status predicted <TM10>
 F:404-420/Domain: transmembrane #status predicted <TM11>

Query Match 4.9%; Score 8; DB 2; Length 443;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 106 LEOLTPAL 113
 11111111
 DB 41 LEOLTPAL 48

RESULT 5
 H90634

Probable transport protein ECS0048 [imported] - *Escherichia coli* (strain O157:H7, sub

C.Species: *Escherichia coli*

C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001

C.Accession: H90634

R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
 gasawara, N.; Yasunaga, T.; Kuwara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A>Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and 9

A.Reference number: A99629; MUID:21156231; PMID:11258796

A.Accession: H90634

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-443 <HAY>

A.Cross-references: GB:BA000007; PIDN:BA83471.1; PID:q13359504; GSPDB:GN001154

A.Experimental source: strain O157:H7, substrain RMD 050952

C.Genetics:

A.Gene: ECS0048

C.Superfamily: yaau protein

Query Match 4.9%; Score 8; DB 2; Length 443;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 106 LEOLTPAL 113
 11111111
 DB 41 LEOLTPAL 48

RESULT 6
 H85485

Probable transport protein yaau [imported] - *Escherichia coli* (strain O157:H7, substr

C.Species: *Escherichia coli*

C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C.Accession: H85485

R.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
 11ler, L.; Grobeck, E.J.; Davis, N.W.; Llm, A.; Diallanta, E.; Potamousis, K.; Apoda

Nature 409, 529-533, 2001

A>Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A.Reference number: A85480; MUID:21074935; PMID:11206551

A.Accession: H85485

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-443 <STO>

A.Cross-references: GB:AE005174; NID:q12512735; PIDN:AAG54348.1; GSPDB:GN00115; UWGP:

A.Experimental source: strain O157:H7, substrain EDL933

C.Genetics:

A.Gene: yaau

C.Superfamily: yaau protein

```
Query Match          4.9%; Score 8; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 LEOLTPAL 113
|||||
Db 41 LEOLTPAL 48

RESULT 7
T04136
cell death suppressor protein 11s1 - maize
N:Alternate names: lethal leaf-spot 1
C:Species: Zea mays (maize)
C>Date: 23-Apr-1999 #sequence_revision 20-Aug-1999 #text_change 21-Jul-2000
C:Accession: T04136; T04133
R:Gray, J.; Close, P. S.; Briggs, S. P.; Johal, G. S.
Cell 89, 25-31, 1997
A:Title: A novel suppressor of cell death in plants encoded by the 11s1 gene of maize.
A:Reference number: Z15232; MUID:97248483
A:Accession: T04136
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-505 <GRA1>
A:Cross-references: EMBL:U77346; NID:g1935910; PIDN:AAC49678.1; PID:g1935912
A:Accession: T04133
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 54-403; 'E', 405-443; 'HT', 446-497; 'V', 499-520 <GRA>
A:Cross-references: EMBL:U77345; NID:g1935908; PIDN:AAC49676.1; PID:g1935909
A:Experimental source: strain pa405 inbred line; leaf
C:Genetics:
A:Gene: 11s1
A:Map position: 15
A:introns: 123/3; 202/2; 244/3; 290/2; 343/3; 436/3
C:Superfamily: Rieske [2Fe-2S] homology
C:Keywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein
F:105-153/Domain: Rieske [2Fe-2S] homology <RSK>
F:115,117,135,138/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status F

Query Match          4.9%; Score 8; DB 2; Length 520;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 PTQELAPS 155
|||||
Db 422 PTQELAPS 429

RESULT 8
T08423
Axin homolog Ax11 - rat
N:Alternate names: Ax11
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08423
R:Yamamoto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi, A.
Mol. Cell. Biol. 18, 2867-2875, 1998
A:Title: Ax11, a member of the Axin family, interacts with both glycogen synthase kinase
A:Reference number: Z16414; MUID:98226558
A:Accession: T08423
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-838 <YAM>
A:Cross-references: EMBL:AF017757; NID:g3080758; PIDN:AAC40089.1; PID:g3080759
A>Note: interacts with GSK-3beta and beta-catenin
C:Keywords: phosphoprotein; signal transduction

Query Match          4.9%; Score 8; DB 2; Length 838;
Best Local Similarity 100.0%; Pred. No. 7.6;
```

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATASVRS 17
|||||
Db 257 ATASVRS 264

RESULT 9
B31443
ovomucoid, third domain - western marsh harrier (fragment)
C:Species: Circus aeruginosus (western marsh harrier)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 07-Feb-1997
C:Accession: B31443
R:Laskowski Jr., M.; Kato, I.; Ardelt, W.; Cook, J.; Denton, A.; Empie, M.W.; Kohr, W.
A:Wieczorek, M.
Biochemistry 26, 202-221, 1987
A:Title: Ovomucoid third domains from 100 avian species: isolation, sequences, and hy
A:Reference number: A90515; MUID:87157615
A:Accession: B31443
A:Molecule type: protein
A:Residues: 1-54 <LAS>
A>Note: the authors designate this sequence with the code OMMAH3
C:Superfamily: ovomucoid; Kazal proteinase inhibitor homology
C:Keywords: egg white; glycoprotein; serine proteinase inhibitor
F:4-54/Domain: Kazal proteinase inhibitor homology <KPI>
F:6-36,14-33,22-54/Disulfide bonds: #status predicted
F:43/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match          4.3%; Score 7; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 NGTISLS 55
|||||
Db 43 NGTISLS 49

RESULT 10
H61588
ovomucoid (PSII-type proteinase inhibitor), third domain - hoatzin
C:Species: Opisthocomus hoazin (hoatzin)
C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 17-Mar-1999
C:Accession: H61588; A44435
R:Apóstol, I.; Gileto, A.; Komiyama, T.; Zhang, W.; Laskowski Jr., M.
J. Protein Chem. 12, 419-433, 1993
A:Title: Amino acid sequences of ovomucoid third domains from 27 additional species o
A:Reference number: A61587; MUID:94072078
A:Accession: H61588
A:Molecule type: protein
A:Residues: 1-54 <APO>
C:Superfamily: ovomucoid; Kazal proteinase inhibitor homology
C:Keywords: serine proteinase inhibitor
F:4-54/Domain: Kazal proteinase inhibitor homology <KPI>
F:6-36,14-33,22-54/Disulfide bonds: #status predicted

Query Match          4.3%; Score 7; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 NGTISLS 55
|||||
Db 43 NGTISLS 49

RESULT 11
T49624
hypothetical protein B5022.60 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C:Accession: T49624
R:Schulte, U.; Aign, V.; Hohnsels, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
```

submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022

A:Accession: T49624

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-147 <SCH>

A:Cross-references: EMBL:AL355932; GSPDB:GN00116; NCSP:B5022.60

A:Experimental source: BAC clone B5022; strain OR74A

C:Genetics:

A:Gene: NCSP:B5022.60

A:Map position: 6

C:Superfamily: Neurospora crassa hypothetical protein B5022.60

Query Match 4.3%; Score 7; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 59 CSRPNE 65
|||||||
DB 30 CSRPNE 36

RESULT 12

hypothetical protein PA0907 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: F83531

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laidig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: AB2950; MWID:20437337

A:Accession: F83531

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-176 <STO>

A:Cross-references: GB:AE004525; GB:AE004091; NID:g9946805; PIDN:AG04296.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA0907

Query Match 4.3%; Score 7; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 SPIHL 81
|||||||

DB 40 SPIHL 46

RESULT 13

hypothetical protein RV0330c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: C70527

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MWID:98293987

A:Accession: C70527

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-246 <COI>

A:Cross-references: GB:Z96800; GB:AL123456; NID:g3261800; PIDN:CAB09578.1; PID:e321793;

A:Experimental source: strain H37RV

C:Genetics:
A:Gene: RV0330c

Query Match 4.3%; Score 7; DB 2; Length 246;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 142 LRATLPP 148
|||||||
DB 106 LRATLPP 112

RESULT 14

fructose-1,6-bisphosphate aldolase class II - Aquifex aeolicus

C:Species: Aquifex aeolicus

C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 22-Jun-1999

C:Accession: A70421

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;

V.

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MWID:98196866

A:Accession: A70421

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-310 <AOE>

A:Cross-references: GB:AE000737; NID:g2983782; PIDN:AC07345.1; PID:g2983787; GB:AE00

A:Experimental source: strain VF5

C:Genetics:

A:Gene: fba

C:Superfamily: fructose-bisphosphate aldolase II

Query Match 4.3%; Score 7; DB 2; Length 310;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 121 VLVDPEQ 127
|||||||
DB 151 VLVDPEQ 157

RESULT 15

muslin JUI10 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1999

C:Accession: S37595; S35048

R:Aubert, J.

submitted to the EMBL Data Library, September 1993

A:Reference number: S37593

A:Accession: S37595

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-330 <ADU>

A:Cross-references: EMBL:X74956; NID:g407052; PIDN:CA52911.1; PID:g407053

R:Dufoess, J.; Porchet, N.; Audie, J.P.; Guyonnet Duperrat, V.; Laine, A.; Van-Seuning

Biochem. J. 293, 329-337, 1993

A:Title: Degenerate 87-base-pair tandem repeats create hydrophilic/hydrophobic altern

A:Reference number: S35047; MWID:93343858

A:Accession: S35048

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-330 <DUF>

Query Match 4.3%; Score 7; DB 2; Length 330;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TTTAATA 12

Db 34 |||||
TTTATA 40

Search completed: October 9, 2002, 02:25:38
Job time: 5269 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2002, 22:31:48 ; Search time 19.91 Seconds
(Without alignments)
201.195 Million cell updates/sec

Title: US-09-786-130-1
Perfect score: 164
Sequence: 1 TPVSQTTATATASVRSKDP.....TLPTQALPSSHPQOG 164

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 231628 segs, 24425594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	4.9	520	4	US-08-810-009-2
2	7	4.3	50	1	US-08-063-551A-2
3	7	4.3	50	3	US-08-926-842B-50
4	7	4.3	116	1	US-08-478-039-103
5	7	4.3	116	1	US-08-476-349A-103
6	7	4.3	275	2	US-08-578-709-13
7	7	4.3	385	4	US-09-036-987A-19
8	7	4.3	385	4	US-09-370-700-19
9	7	4.3	403	4	US-08-861-774E-27
10	7	4.3	406	4	US-08-861-774E-25
11	7	4.3	407	4	US-08-861-774E-28
12	7	4.3	500	2	US-08-578-709-15
13	6	3.7	10	4	US-09-238-448-1
14	6	3.7	10	4	US-09-238-448-5
15	6	3.7	14	2	US-07-876-941A-36
16	6	3.7	49	3	US-08-926-842B-49
17	6	3.7	57	1	US-08-162-102C-38
18	6	3.7	84	3	US-08-906-769-99
19	6	3.7	84	3	US-08-906-616-99
20	6	3.7	84	4	US-08-817-795-99
21	6	3.7	84	4	US-08-639-075A-99
22	6	3.7	84	4	US-09-012-431-99
23	6	3.7	84	4	US-09-012-692-99
24	6	3.7	84	4	US-08-906-613-99
25	6	3.7	84	5	PCT-US95-14442A-99
26	6	3.7	93	3	US-08-894-699-63
27	6	3.7	93	4	US-09-444-410-63

28	6	3.7	94	3	US-08-894-699-62	Sequence 62, App1
29	6	3.7	94	3	US-08-894-699-64	Sequence 64, App1
30	6	3.7	94	4	US-09-444-410-62	Sequence 62, App1
31	6	3.7	94	4	US-09-444-410-64	Sequence 64, App1
32	6	3.7	96	4	US-09-228-986-98	Sequence 98, App1
33	6	3.7	97	3	US-08-894-699-26	Sequence 26, App1
34	6	3.7	97	3	US-08-894-699-27	Sequence 27, App1
35	6	3.7	97	3	US-08-894-699-30	Sequence 30, App1
36	6	3.7	97	4	US-09-444-410-26	Sequence 26, App1
37	6	3.7	97	4	US-09-444-410-27	Sequence 27, App1
38	6	3.7	97	4	US-09-444-410-30	Sequence 30, App1
39	6	3.7	99	3	US-08-894-699-31	Sequence 31, App1
40	6	3.7	99	3	US-08-894-699-34	Sequence 34, App1
41	6	3.7	99	4	US-09-444-410-31	Sequence 31, App1
42	6	3.7	99	4	US-09-444-410-34	Sequence 34, App1
43	6	3.7	104	1	US-08-276-852-94	Sequence 94, App1
44	6	3.7	104	1	US-08-276-852-100	Sequence 100, App
45	6	3.7	104	1	US-08-899-575-94	Sequence 94, App1

ALIGNMENTS

RESULT 1
US-08-810-009-2
; Sequence 2, Application US/08810009
; Patent No. 6211437
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: John, Gurmuth S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
; TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; City: Charlotte
; STATE: No. 6211437th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,009
; FILING DATE: 04-MAR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Spullin, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 5718-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELETYPE: 575102
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 520 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-810-009-2

Query Match 4.9%; Score 8; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 148 PTOFALPS 155
|||||||

Db 422 PROEALPS 429

RESULT 2

US-08-063-551A-2

; Sequence 2, Application US/08063551A
; Patent No. 5434071

GENERAL INFORMATION:

APPLICANT: ROSENBERG, Eugene

APPLICANT: SROHAM, Yuval

TITLE OF INVENTION: Preparation exhibiting enzymatic

TITLE OF INVENTION: delignification activity, a method of

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESS: BACON & THOMAS

STREET: 625 Slaters Lane - 4th Floor

CITY: Alexandria

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 1.2mb storage

COMPUTER: IBM AT COMPATIBLE

OPERATING SYSTEM: MS-DOS 5.0

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/063.551A

FILING DATE: 19930518

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 854645

FILING DATE: 02-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Richard E. Fichter

REGISTRATION NUMBER: 26,382

REFERENCE/DOCKET NUMBER: REF/Rosenberg/551

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-683-0500

TELEFAX: 703-683-1080

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 50 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: N-terminal fragment

US-08-063-551A-2

Query Match

Best Local Similarity 4.3%; Score 7; DB 1; Length 50;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 74 GSFIEHL 80

Db 24 GSFIEHL 30

RESULT 3

US-08-926-842B-50

; Sequence 50, Application US/08926842B

; Patent No. 6030807

GENERAL INFORMATION:

APPLICANT: Sa-No. 6030807neira, Isabel

APPLICANT: de Lencastre, Herminda

TITLE OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESS: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/926.842B

FILING DATE: 10-SEP-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-089 N

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 50 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

US-08-926-842B-50

Query Match

Best Local Similarity 4.3%; Score 7; DB 3; Length 50;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 74 GSFIEHL 80

Db 24 GSFIEHL 30

RESULT 4

US-08-478-039-103

; Sequence 103, Application US/08478039

; Patent No. 5681722

GENERAL INFORMATION:

APPLICANT: Newman, Roland A.

APPLICANT: Raab, Ronald W.

TITLE OF INVENTION: Recombinant Antibodies for Human Therapy

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESS: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince St.

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478.039

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/379,072

FILING DATE: 25-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/912,292

FILING DATE: 10-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: #9
US-08-478-039-103

Query Match 4.3%; Score 7; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 LSLSCVA 58
|||||||
DB 18 LSLSCVA 24

RESULT 5
US-08-476-349A-103
Sequence 103, Application US/08476349A
Patent No. 5750105
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991

ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: #9
US-08-476-349A-103

Query Match 4.3%; Score 7; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 LSLSCVA 58
|||||||
DB 18 LSLSCVA 24

RESULT 6
US-08-578-709-13
Sequence 13, Application US/08578709
Patent No. 5814509
GENERAL INFORMATION:
APPLICANT: TANABE, Tadashi
TITLE OF INVENTION: PROSTACYCLIN SYNTHASE DERIVED FROM HUMAN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,709
FILING DATE: 28-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/00838
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 114316/1994
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gubinsky, Louis
REGISTRATION NUMBER: 24,835
REFERENCE/DOCKET NUMBER: Q40439
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-578-709-13

Query Match 4.3%; Score 7; DB 2; Length 275;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PVSQTTT 8
|||||
DB 98 PVSQTTT 104

RESULT 7

US-09-036-987A-19
; Sequence 19, Application US/09036987A
; Patent No. 6143526
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Broughton, Mary C.
; APPLICANT: Crawford, Kathryn P.
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Merlo, Donald J.
; APPLICANT: Turner, Jan R.
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dow Agrosciences LLC Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,987A
; FILING DATE: 09-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R.
; REGISTRATION NUMBER: 28,479
; REFERENCE/DOCKET NUMBER: 50,608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317)337-4816
; TELEFAX: (317)337-4847
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-036-987A-19

Query Match 4.3%; Score 7; DB 4; Length 385;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123 VDEQVY 129
|||||
DB 45 VDEQVY 51

RESULT 8

US-09-370-700-19
; Sequence 19, Application US/09370700
; Patent No. 6274350

; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Broughton, Mary C.
; APPLICANT: Crawford, Kathryn P.
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patli J.
; APPLICANT: Turner, Jan R.
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 DIV1
; CURRENT APPLICATION NUMBER: US/09/370,700
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/36987
; EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO: 19
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-19

Query Match 4.3%; Score 7; DB 4; Length 385;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123 VDEQVY 129
|||||
DB 45 VDEQVY 51

RESULT 9

US-08-861-774E-27
; Sequence 27, Application US/08861774E
; Patent No. 6297007
; GENERAL INFORMATION:
; APPLICANT: Waters, Barbara
; APPLICANT: Miao, Vivian
; APPLICANT: Ho, Yap
; APPLICANT: Tong, Seow
; TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
; FILE REFERENCE: 9993-006
; CURRENT APPLICATION NUMBER: US/08/861,774E
; CURRENT FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO: 27
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: KS beta gene
US-08-861-774E-27

Query Match 4.3%; Score 7; DB 4; Length 403;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 EHLPGRL 84
|||||
DB 59 EHLPGRL 65

RESULT 10

US-08-861-774E-25
; Sequence 25, Application US/08861774E
; Patent No. 6297007
; GENERAL INFORMATION:
; APPLICANT: Waters, Barbara
; APPLICANT: Miao, Vivian

APPLICANT: Ho, Yap
APPLICANT: Tong, Seow
TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
TITLE OF INVENTION: BIOACTIVE MOLECULES
FILE REFERENCE: 9993-006
CURRENT APPLICATION NUMBER: US/08/861,774E
CURRENT FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 406
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: KS beta gene
US-08-861-774E-25

Query Match 4.3%; Score 7; DB 4; Length 406;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 EHLPGRL 84
|||||
Db 60 EHLPGRL 66

RESULT 11
US-08-861-774E-28
Sequence 28, Application US/08861774E
Patent No. 6297007
GENERAL INFORMATION:
APPLICANT: Waters, Barbara
APPLICANT: Miao, Vivian
APPLICANT: Ho, Yap
TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
TITLE OF INVENTION: BIOACTIVE MOLECULES
FILE REFERENCE: 9993-006
CURRENT APPLICATION NUMBER: US/08/861,774E
CURRENT FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 407
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: KS beta gene
US-08-861-774E-28

Query Match 4.3%; Score 7; DB 4; Length 407;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 EHLPGRL 84
|||||
Db 60 EHLPGRL 66

RESULT 12
US-08-578-709-15
Sequence 15, Application US/08578709
Patent No. 5814509
GENERAL INFORMATION:
APPLICANT: TANABE, Tadashi
TITLE OF INVENTION: PROSTACYCLIN SYNTHASE DERIVED FROM HUMAN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,709
FILING DATE: 28-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/00838
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 114316/1994
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gubinsky, Louis
REGISTRATION NUMBER: 24,835
REFERENCE/DOCKET NUMBER: Q40439
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-578-709-15

Query Match 4.3%; Score 7; DB 2; Length 500;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PVSQTTT 8
|||||
Db 323 PVSQTTT 329

RESULT 13
US-09-238-448-1
Sequence 1, Application US/09238448
Patent No. 6238925
GENERAL INFORMATION:
APPLICANT: Sampson, Hugh A.
TITLE OF INVENTION: Method for Determining Likelihood of Developing
FILE REFERENCE: HS 100
CURRENT APPLICATION NUMBER: US/09/238,448
CURRENT FILING DATE: 1999-01-28
EARLIER APPLICATION NUMBER: 60/073,171
EARLIER FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-238-448-1

Query Match 3.7%; Score 6; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 59 CSRFPN 64
|||||

Db 5 CSRFPPN 10

RESULT 14

US-09-238-448-5
Sequence 5, Application US/09238448

Patent No. 6238923

GENERAL INFORMATION:

APPLICANT: Sampson, Hugh A.

TITLE OF INVENTION: Method for Determining Likelihood of Developing
FILE OF INVENTION: Immunological Tolerance

FILE REFERENCE: HS 100

CURRENT APPLICATION NUMBER: US/09/238,448

CURRENT FILING DATE: 1999-01-28

EARLIER APPLICATION NUMBER: 60/073,171

EARLIER FILING DATE: 1998-01-30

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 5

LENGTH: 10

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: peptide

US-09-238-448-5

Query Match

Best Local Similarity 3.7%; Score 6; DB 4; Length 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 CSRFPPN 64

Db 3 CSRFPPN 8

RESULT 15

US-07-876-941A-36

Sequence 36, Application US/07876941A

Patent No. 5885768

GENERAL INFORMATION:

APPLICANT: Reyes, Gregory R.

APPLICANT: Bradley, Daniel W.

APPLICANT: Tam, Albert W.

APPLICANT: Mitchell, Carl

TITLE OF INVENTION: Hepatitis E Virus Peptide Antigen and

TITLE OF INVENTION: Antibodies

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

ADDRESSEE: Denlinger & Associates

STREET: 350 Cambridge Avenue, Suite 250

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/876,941A

FILING DATE: 01-MAY-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 822,335

FILING DATE: 17-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 505,888

FILING DATE: 05-APRIL-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 420,921

FILING DATE: 13-OCTOBER-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 367,486

FILING DATE: 16-JUNE-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 336,672

FILING DATE: 11-APRIL-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 208,997

FILING DATE: 17-JUNE-1988

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 38,615

REFERENCE/DOCKET NUMBER: 4600-0093.33

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Fig. 11, ORF 2, aa 341-354

US-07-876-941A-36

Query Match

Best Local Similarity 3.7%; Score 6; DB 2; Length 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TTTAAT 11

Db 2 TTTAAT 7

Search completed: October 9, 2002, 01:47:15
Job time: 11727 sec